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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 25, 2004, 09:15:20 ; Search time 53.5 Seconds
(without alignments)
5365.762 Million cell updates/sec

Title: US-09-914-324A-3

Sequence: 1 cccaataatgcgcgcagcagat.....aaagtcacgttcgattcgcg 508

Scoring table:

BIOSIM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Rgapop 6.0, Rgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=x1p
-O=/cgn2.1/USPRO.spool.p/US09914324/runat.25032004.090846.8708/app.query.fasta_1.647
-DB-A=Geneseq.29Jan04 -OPMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNIT=bits -START=1 -END=-1 -MATRIX=blosome62 -TRANS=human40.cdi
-LIST=45 -DOCALLIG=200 -THR.SCORE=Pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NCRM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09914324 @CGN.1.1.81 @runat.25032004.090846.8708 -NCPU=6 -ICPU=3
-NO.MAP -LARGEQUERRY -NEG.SCORSE=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: A_Geneseq.29Jan04:

1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	616	64.0	108	3	AA019160 Amino aci
2	616	64.0	108	3	AA008813 A human c
3	616	64.0	108	3	AA003890 Human sec
4	616	64.0	108	4	AA047599 ROCI. 1/2
5	616	64.0	108	5	AA024620 Human RIN
6	616	64.0	108	7	ADC02481 RING fing
7	534	55.5	108	4	AB068080 Drosophi1
8	514.5	53.5	118	3	AA023004 Arabidops
9	511	53.1	109	3	AA023005 Arabidops
10	400.5	41.6	122	4	AB066109 Drosophi1

11	385	40.0	121	3	AA008814 A Yeast C
12	323	32.6	57	3	AA041007 Human ORF
13	294	30.6	118	4	AA015873 Human nov
14	294	30.6	118	6	AB054942 Human nov
15	292	30.4	113	3	AA043295 Human ORF
16	292	30.4	113	3	AA016332 Human nov
17	292	30.4	131	6	AB055401 Human nov
18	292	30.2	131	6	AA006509 Human sen
19	291	30.2	113	2	AA006491 Amino aci
20	290.5	30.2	113	2	AA019161 Amino aci
21	290.5	30.2	113	3	AA047600 ROCI. 1/2
22	287	29.8	113	5	AA024621 Human RIN
23	287	29.8	113	7	ADC02483 RING fing
24	287	29.8	113	7	AA006508 Human sen
25	285	29.6	113	2	AA006500 Human sen
26	283	29.4	113	2	AA006501 Human sen
27	283	29.4	113	2	AA006498 Human sen
28	282	29.3	113	2	AA006495 Human sen
29	282	29.3	113	2	AA006503 Human sen
30	282	29.3	113	2	AA006502 Human sen
31	282	29.3	113	2	AA006506 Human sen
32	282	29.3	113	2	AA006495 Human sen
33	282	29.3	113	2	AA006498 Human sen
34	282	29.3	113	2	AA006505 Human sen
35	282	29.3	113	2	AA006504 Human sen
36	274	28.5	113	2	AA006497 Human sen
37	272	28.3	113	2	AA006507 Human sen
38	272	28.3	113	2	AA006507 Human sen
39	235	24.4	97	2	AA043284 Human ORF
40	235	24.4	97	3	AB022655 Novel hum
41	218	23.7	43	4	AB022655 Novel hum
42	218	23.7	43	4	AB022655 Novel hum
43	214.5	22.3	124	4	AA016331 Human nov
44	214.5	22.3	124	6	AB055400 Human nov
45	213	22.1	88	3	AA058912 Breast an

ALIGNMENTS

RESULT 1	AA019160 standard; protein; 108 AA.
AA019160	
ID	AA019160;
AC	AA019160;
DT	19-FEB-2001 (first entry)
XX	
DE	Amino acid sequence of human ring finger protein ROCI.
XX	
KM	ROCI; ROCI; cullin; ring finger protein; APC11; APC complex; SCF pathway;
KW	cullin dependent ubiquitin ligase; CDK inhibitor Sic1 degradation;
KW	tumour.
OS	Homo sapiens.
XX	
PN	WO200058472-A2.
PD	05-OCT-2000.
XX	
PF	31-MAR-2000; 2000MO-US008592.
XX	
PR	31-MAR-1999; 99US-0127261P.
PR	22-NOV-1999; 99US-0166927P.
PA	(UYNC-) UNIV NORTH CAROLINA.
PI	Xiong Y, Ohta T;
XX	
DR	WPI, 2000-647235/62.
XX	N-PSDE; AAA68882.
PT	Novel nucleic acid encoding cullin regulating ring finger proteins,
PT	termed as ROC proteins similar to anaphase-promoting complex 11, for

XX 06-OCT-2000 (first entry)
 DT Human secreted protein, SEQ ID NO: 7971.
 XX
 DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 XX gene therapy; chromosome mapping.
 XX
 OS Homo sapiens.
 XX
 PN EPI033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-00200610.
 XX
 PR 26-FEB-1999; 99US-0122487P.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclet A, Giordano J;
 XX
 DR WPI; 2000-500381/45.
 XX
 DR N-PSDB; AAC03896.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX
 PS Claim 13; SEQ ID NO 7971; 71bp + Sequence Listing; English.
 XX
 CC The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 XX
 SQ Sequence 108 AA;
 XX
 Alignment Scores:
 Pred. No.: 3,43e-67 Length: 108
 Score: 616.00 Matches: 108
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 64.03% Indels: 0
 DB: 3 Gaps: 0
 US-09-914-324a-3 (1-508) x AAG03890 (1-108)
 QY 7 ATGGCGGAGCGATGATGATGATACCCCGAGCGGACCAACAGCGGCGGCGCAAG 66
 DB 1 MetAlaAlaAlaMetLaspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
 QY 67 CGCTTTGAAGTGAAGAAAAGTGAATGCGATGACCTTCGGGCTTGGGATATTGGCTTGA 126
 DB 21 ArpHeGluValLysLysLysTPAsnAlaValAlaLeuTPAlaItrpAspIleValValAsp 40
 QY 127 AACTGTGCATCTGTGAGGAACACATTAATGATCTTTCATAGATGATCAAGCTAAC 186
 DB 41 AsnCySerAlaIleCysArgAsnHisIleMetAspLeuCySileGluCysGlnAlaAsnGln 60
 QY 187 GCGTCCGCTACTTCAAGAAAGTGTACTGTCGCATGGGAGAGTCTGTAAACCATGCTTTTAC 246
 DB 61 AlaSerAlaItrpSerGluGluCysThrValAlaItrpGlyValCysAsnHisAlaPheHis 80

QY 247 TTCGACTGCATCTCTCGCTGGCTGCTCAAAACAGCAGAGTGTCCATTGGACACAGAGAG 306
 DB 81 PheHisCysIleSerAlaItrpLeuLysTrpArgGlnValCysProLeuAspAsnArgGln 100
 QY 307 TGGGAATTCCAAAAGTATGGGCGAC 330
 DB 101 TrpGluPheGlnLysTrpGlyHis 108
 RESULT 4
 ID AAB47599 standard; protein; 108 AA.
 XX
 AC AAB47599;
 XX
 DT 07-JAN-2002 (first entry)
 XX
 DE R001.
 XX
 KW Assay; ubiquitin ligase; tag1-ubiquitin; E1; E2;
 KW ubiquitin activating enzyme; ubiquitin conjugating enzyme; E3;
 KW ubiquitin ligase; ubiquitination modulator.
 XX
 OS Unidentified.
 XX
 PN MO200175145-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 03-APR-2001; 2001WO-US010906.
 XX
 PR 03-APR-2000; 2000US-00542497.
 XX
 PA (RIGE-) RIGEL PHARM INC.
 XX
 PI Isekhani SD, Huang J, Sheung J, Pray TR;
 XX
 DR WPI; 2001-626445/72.
 XX
 PT Assaying ubiquitin ligase activity for identifying modulators of
 PT ubiquitination, by combining ubiquitin, ubiquitin activating conjugating
 PT enzyme, ubiquitin ligase and measuring amount of ubiquitin bound to the
 PT ligase.
 XX
 PS Example 1; Fig 11; 98pp; English.
 XX
 CC The sequences given in AAB47596-602 are proteins which may be used in the
 CC method of the invention for assaying ubiquitin ligase activity. The
 CC method comprises combining under conditions that favour ubiquitin ligase
 CC activity, tag1-ubiquitin, E1 (ubiquitin activating enzyme), E2 (ubiquitin
 CC conjugating enzyme) and E3 (ubiquitin ligase) and measuring the amount of
 CC tag1-ubiquitin bound to the E3. The method is useful for assaying
 CC ubiquitin ligase activity and ubiquitination enzyme activity which is
 CC useful for identifying ubiquitination modulator. The method comprises
 CC combining tag1-ubiquitin, the modulator, E1, E2 and tag2-E3 and measuring
 CC the amount of tag1-ubiquitin bound to tag2-E3 or combining tag1-
 CC ubiquitin, modulator, E1 and tag2-E2 and measuring the amount of tag1-
 CC ubiquitin bound to tag2-E2. Ubiquitin ligase activity is measured
 CC directly, eliminating the need for target proteins and subsequent
 CC analysis such as separating ligated from unligated material in an SDS-
 CC PAGE procedure. This allows multi-well array analysis and high throughput
 CC screening techniques for modulators of ubiquitination activity. The
 CC method also allows the analysis of many different combinations of E3
 CC components and E2/E3 combinations without requiring prior identification
 CC of specific target substrates. Ubiquitin is labeled, directly or
 CC indirectly and this allows for easy and rapid detection and measurement
 CC of ligated ubiquitin
 XX
 SQ Sequence 108 AA;
 XX
 Alignment Scores:
 Pred. No.: 3,43e-67 Length: 108
 Score: 616.00 Matches: 108
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 64.03% Indels: 0
 DB: 4 Gaps: 0

US-09-914-324a-3 (1-508) x AAB47559 (1-108)

QY 7 ATGGCGGCGAGATGATGTGATATCCCGAGCGGACCAACAGCGCGCGGACAGAG 66
 Db 1 MetAlaAlaIaMeIaAspValAspThrProSerGlyThrAsnSerGlyAlaGlyIys 20
 QY 67 CGCTTTGAAGTGAAGAAAAGTGAATGCAGTACCCCTCGGGCTGGATTTGGTTGAT 126
 Db 21 ArgPheGluValIysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
 QY 127 AACTGTGCCATCTGCAGGAGACCACTATGAGATCTTTGCATAGATGATCAAGTAAACCAG 186
 Db 41 AsnCySAIaIleCyArgAsnHisIleMetAspLeuCySileGlyCysGlnAlaAsnGln 60
 QY 187 GCGTCGCTACTTTCAGAAAGTGTACTGTCCGATGGGAGTCTGAACATGCTTTTAC 246
 Db 61 AlaSerAlaThrSerGluGluCysThrValAlaIleTrpGlyValCysAsnHisAlaPheHis 80
 QY 247 TTCACATGCATCTCTCGCTGGCTCAAAACAGACAGAGTGTCTCCATTGAGCAACAGAG 306
 Db 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGln 100
 QY 307 TGGGAATTCCAAAGTATGGGCAC 330
 Db 101 TrpGluPheGlnLysTrpGlyHis 108

RESULT 5

AAB24620
 ID AAB24620 standard; protein; 108 AA.

AAE24620;
 AC 22-OCT-2002 (first entry)

DE Human RING finger protein, ROC1.
 XX Ubiquitin ligase; UL; tag1-ubiquitin; E1; ubiquitin-activating enzyme;
 KM E2; ubiquitin-conjugating enzyme/ubiquitin carrier protein; E3; human;
 KM RING finger protein.

OS Homo sapiens.
 XX US2002042083-A1.
 PN 11-APR-2002.
 PD 03-APR-2001; 2001US-00826312.
 PF 03-APR-2000; 2000US-00542497.
 PR (RIGF-) RIGEL PHARM INC.
 PA Issakani SD, Huang J, Sheung J, Pray TR;
 PI Tssakani SD, Huang J, Sheung J, Pray TR;
 XX WPI; 2002-488718/52.

DR WPI; 2002-488718/52.
 XX Assay for ubiquitin ligase activity, useful for identifying modulators,
 PT by measuring binding of labeled ubiquitin to ubiquitin ligase.

XX Disclosure; Fig 11; 56pp; English.
 XX The invention relates to an assay for ubiquitin ligase (UL) activity
 CC which comprises incubating tag1-ubiquitin, E1 (ubiquitin-activating
 CC enzyme), E2 (ubiquitin-conjugating enzyme/ubiquitin carrier protein) and
 CC E3 (UL) and measuring the amount of tag1-ubiquitin bound to E3. The
 CC method is particularly used to screen for modulators of UL activity. The
 CC present sequence is human RING finger protein, ROC1

XX Sequence 108 AA;
 SQ

Alignment Scores:
 Pred. No.: 3,43e-67 Length: 108
 Score: 616.00 Matches: 108
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 64.03% Indels: 0
 DB: 5 Gaps: 0

US-09-914-324a-3 (1-508) x AAB24620 (1-108)

QY 7 ATGGCGGCGAGATGATGTGATATCCCGAGCGGACCAACAGCGCGCGGACAGAG 66
 Db 1 MetAlaAlaIaMeIaAspValAspThrProSerGlyThrAsnSerGlyAlaGlyIys 20
 QY 67 CGCTTTGAAGTGAAGAAAAGTGAATGCAGTACCCCTCGGGCTGGATTTGGTTGAT 126
 Db 21 ArgPheGluValIysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
 QY 127 AACTGTGCCATCTGCAGGAGACCACTATGAGATCTTTGCATAGATGATCAAGTAAACCAG 186
 Db 41 AsnCySAIaIleCyArgAsnHisIleMetAspLeuCySileGlyCysGlnAlaAsnGln 60
 QY 187 GCGTCGCTACTTTCAGAAAGTGTACTGTCCGATGGGAGTCTGAACATGCTTTTAC 246
 Db 61 AlaSerAlaThrSerGluGluCysThrValAlaIleTrpGlyValCysAsnHisAlaPheHis 80
 QY 247 TTCACATGCATCTCTCGCTGGCTCAAAACAGACAGAGTGTCTCCATTGAGCAACAGAG 306
 Db 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGln 100
 QY 307 TGGGAATTCCAAAGTATGGGCAC 330
 Db 101 TrpGluPheGlnLysTrpGlyHis 108

RESULT 6

ADC02481
 ID ADC02481 standard; protein; 108 AA.

AC ADC02481;
 XX 18-DEC-2003 (first entry)

DE RING finger protein ROC1.
 XX Ubiquitin; Mdm2; p53; RING finger protein; ROC1.
 KM Ubiquitin; Mdm2; p53; RING finger protein; ROC1.

OS Unidentified.
 XX US2003104474-A1.
 PN 05-JUN-2003.
 PD 26-MAR-2002; 2002US-00108767.
 PF 03-APR-2000; 2000US-00542487.
 PR 03-APR-2001; 2001US-00826312.
 PR 04-MAR-2002; 2002US-00091139.

XX (ISSA/) ISSAKANI S D.
 PA (HUAN/) HUANG J.
 PA (SHEU/) SHEUNG J.
 PA (PRAY/) PRAY T R.

XX Issakani SD, Huang J, Sheung J, Pray TR;
 DR WPI; 2003-787056/74.
 XX Assaying for candidate agent that modulates attachment of ubiquitin
 PT moiety to Mdm2 protein comprises combining ubiquitin agent comprising
 PT ubiquitin moiety, Mdm2 protein, and candidate agent.

XX Disclosure; Fig 11; 96pp; English.
 PS

XX The present sequence represents a method of assaying for a candidate
CC agent that modulates the attachment of a ubiquitin moiety to an Mdm2
CC protein. The method is useful for assaying for a candidate agent that
CC modulates the attachment of a ubiquitin moiety to an Mdm2 or p53 protein.
CC The present sequence represents the amino acid sequence of RING finger
CC protein ROC1.
XX
SQ Sequence 108 AA;
XX
Alignment Scores:
Pred. No.: 3,43e-67 Length: 108
Score: 616.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 64.03% Indels: 0
DB: 7 Gaps: 0
US-09-914-324A-3 (1-508) x ADC02481 (1-108)
QY 7 ATGCGCGAGCGATGATGATGATACCCGAGCGGACCAAGCGCGCGGCAAGAG 66
Db 1 MetAlAlAlAlMetAspValAspThrProSerGlyThAsnSerGlyAlaGlyLys 20
QY 67 CGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 126
Db 21 ArgPheGluValLysLysLysLysLysLysLysLysLysLysLysLysLysLys 40
QY 127 AACTGTGCATCTGCAGAACCAATTGATGATGATGATGATGATGATGATGATGATGAT 186
Db 41 AsnGlyAlaIleCysArgAsnHisIleMetAspLeuGlyIleGluCysGlnAlaSerGln 60
QY 187 GCGTCGCTACTCTCAGAAAGTGTACTGTGCGATGGGAGTGTGTAACCATCTTTGAC 246
Db 61 AlaSerAlaThrSerGluGluCysThrValAlaIleGlyValCysAsnHisAlaPheHis 80
QY 247 TTCCATATGATCTCTGCGTGCCTCAACAGACAGAGTGTGTCATTTGACAGAGAG 306
Db 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGln 100
QY 307 TGGGAATTCCTCAAAAGTATGGGCAC 330
Db 101 TrpGluPheGlnLysTrpGlyHis 108
RESULT 7
ABB68080 standard; protein; 108 AA.
XX
AC ABB68080;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polyprotein SEQ ID NO 31032.
XX
KM Drosophila; developmental biology; cell signalling; insecticide;
XX
KM pharmaceutical.
XX
OS Drosophila melanogaster.
XX
FN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
XX
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li FMD, Myers EW,
XX
DR WPI; 2001-656860/75.

DR N-PSDB; ABL12183.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
XX
XX
PS Disclosure; SEQ ID NO 31032; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 108 AA;
XX
Alignment Scores:
Pred. No.: 5.22e-57 Length: 108
Score: 534.00 Matches: 95
Percent Similarity: 90.83% Conservative: 4
Best Local Similarity: 87.16% Mismatches: 6
Query Match: 55.51% Indels: 2
DB: 4 Gaps: 2
US-09-914-324A-3 (1-508) x ABB68080 (1-108)
QY 19 ATGATATGAT-----ACCGGAGCGGACCAACAGCGGCGGCAAG 63
Db 1 MetGluValAspGluAspGlyTrpGluValProSerSerSerLysGly---AspLys 19
QY 64 AAGCGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 123
Db 20 LysArgPheGluValLysLysLysLysLysLysLysLysLysLysLysLysLys 39
QY 124 GATACCTGTGCTCCTCAGAACCAATTGATGATGATGATGATGATGATGATGATGATGAT 183
Db 40 AspAsnGlyAlaIleCysArgAsnHisIleMetAspLeuGlyIleGluCysGlnAlaSer 59
QY 184 CAGCGTCGCTACTCTCAGAAAGTGTACTGTGCGATGGGAGTGTGTAACCATCTTTT 243
Db 60 GlnAlaSerAlaThrSerGluGluCysThrValAlaIleTrpGlyValCysAsnHisAlaPhe 79
QY 244 CACTTCACTGATCTCTCTGCTGCTCAAAACAGACAGAGTGTGTCATTTGACAGAGA 303
Db 80 HisPheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArg 99
QY 304 GAGTGGGAATTCCTCAAAAGTATGGGCAC 330
Db 100 GluTrpAspPheGlnLysTrpGlyHis 108
RESULT 8
AAG23004
ID AAG23004 standard; protein; 118 AA.
XX
AC AAG23004;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26148.
XX
KM Protein identification; signal transduction pathway; metabolic pathway;
XX
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX
KM termination sequence.
XX
OS Arabidopsis thaliana.
XX
FN EP1033405-A2.
XX
PI

Thu Mar 25 10:42:33 2004

us-09-914-324a-3.rag

PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0133487P.
PR 07-MAY-1999; 99US-0133863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137502P.
PR 04-JUN-1999; 99US-0137724P.
PR 07-JUN-1999; 99US-0138094P.
PR 08-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 17-JUN-1999; 99US-0139453P.
PR 18-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139495P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
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PR 13-JUL-1999; 99US-0143542P.
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PR 26-OCT-1999; 99US-0161355P.
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PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161932P.
PR 29-OCT-1999; 99US-0162142P.

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Score: 514.50
Percent Similarity: 83.76%
Best Local Similarity: 78.63%
Query Match: 53,488
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Gaps: 2
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2 AaHthLeuApsSerSspValHrMetIleProAlaGlyAlaLaserSerValAla 21
|||:::|
43 ---ACCAAGAGCGCGCGCGCAAGAGCGCTTGAAGTAAAGTGAAGTGCATCAGCC 99
|||||
22 AaSerSerSerAnLysLysAlaLysArgPheGluIleLysLysTrpSerLValAla 41
|||||
100 CTCGTGGAGCTGGATATTTGGTTGATTAAGTGCATGAGGAGACACATTTGAT 159
|||||
42 LeuTrpAlaTrpPheLValValAlaPheNcySalAlIleCysAlrPheNstIleMetAsp 61
|||||
160 CTTTGATAGATGTCAGGTCACAGGCGTCCGCTACTTCAAGAGTGTACTGTGCA 219
|||||
62 LeuCyAlIleGluLysGlnAlaAsnGlnAlaSerAlaThrSerGlnLincYstrValAla 81
|||||
220 TGGGGAGCTGTATACAGATGTTTCACTTCCACTGCATGCTGTGGCTGCAAAACAGA 279
|||||
82 TrpGlyValAlaLysAsnHsIAlaPheNstIlePheNstIleCysAlrPheNstIleMetAsp 101
|||||
280 CAGGTGTGTCATTTGACACAGAGAGTGGAAATTCGAAAGTATGGGAC 330
|||||
102 GluValCysLeuLeuApsSerSspValHrMetIleProAlaGlyAlaLaserSerValAla 118
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13 GCAGCGATGATGTGATAC-----CCGAGCGGC----- 42
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2 AaHthLeuApsSerSspValHrMetIleProAlaGlyAlaLaserSerValAla 21
|||:::|
43 ---ACCAAGAGCGCGCGCGCAAGAGCGCTTGAAGTAAAGTGAAGTGCATCAGCC 99
|||||
22 AaSerSerSerAnLysLysAlaLysArgPheGluIleLysLysTrpSerLValAla 41
|||||
100 CTCGTGGAGCTGGATATTTGGTTGATTAAGTGCATGAGGAGACACATTTGAT 159
|||||
42 LeuTrpAlaTrpPheLValValAlaPheNcySalAlIleCysAlrPheNstIleMetAsp 61
|||||
160 CTTTGATAGATGTCAGGTCACAGGCGTCCGCTACTTCAAGAGTGTACTGTGCA 219
|||||
62 LeuCyAlIleGluLysGlnAlaAsnGlnAlaSerAlaThrSerGlnLincYstrValAla 81
|||||
220 TGGGGAGCTGTATACAGATGTTTCACTTCCACTGCATGCTGTGGCTGCAAAACAGA 279
|||||
82 TrpGlyValAlaLysAsnHsIAlaPheNstIlePheNstIleCysAlrPheNstIleMetAsp 101
|||||
280 CAGGTGTGTCATTTGACACAGAGAGTGGAAATTCGAAAGTATGGGAC 330
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102 GluValCysLeuLeuApsSerSspValHrMetIleProAlaGlyAlaLaserSerValAla 118
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RESULT 9
AAG23005
ID AAG23005 standard; protein; 109 AA.
XX
AC AAG23005;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26149.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123548P.
XX 23-MAR-1999; 99US-0125788P.
XX 25-MAR-1999; 99US-0126264P.
XX 29-MAR-1999; 99US-0126785P.
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XX 06-APR-1999; 99US-0128234P.
XX 08-APR-1999; 99US-0128714P.
XX 16-APR-1999; 99US-0129845P.
XX 19-APR-1999; 99US-0130077P.
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XX 05-MAY-1999; 99US-0132485P.
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XX 25-MAY-1999; 99US-0136021P.
XX 27-MAY-1999; 99US-0136292P.
XX 28-MAY-1999; 99US-0136782P.
XX 01-JUN-1999; 99US-0137222P.
XX 03-JUN-1999; 99US-0137528P.
XX 04-JUN-1999; 99US-0137502P.
XX 07-JUN-1999; 99US-0137742P.
XX 06-JUN-1999; 99US-0138094P.
XX 10-JUN-1999; 99US-0138540P.
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XX 16-JUN-1999; 99US-0139452P.
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XX 18-JUN-1999; 99US-0139454P.
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XX 18-JUN-1999; 99US-0139457P.
XX 18-JUN-1999; 99US-0139457P.
XX 18-JUN-1999; 99US-0139458P.
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 QY 157 GATCTTTGATAGATATGCTCAAGCTTAACAGCGCTCCGCTACTTCACAAAGAGTCTGTC 216
 Db 52 AspLeuGylleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGlnGluCysThrVal 71
 QY 217 GCATGGGAGTCTGTAAACAATGCTTTCACTTCATGATCTGCTGCTCAAAACA 276
 Db 72 AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuVal 91
 QY 277 CGACAGGTGTGCTGATGACACAGAGTGGAAATTCACAAAGATAGGCGAC 330
 Db 92 ArgGlnValCysProLeuAspAsnSerGluTrpGluPheGlnIleValTyrGlyHis 109
 RESULT 10
 ABB6109
 ID ABB6109 standard; protein; 122 AA.
 AC ABB6109;
 XX
 DT 26-MAR-2002 (first entry)
 DE Drosophila melanogaster polypeptide SEQ ID NO 25119.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 FN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WC-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 XX
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li FWD, Myers EM;
 XX
 DR MPI; 2001-656660/75.
 XX
 DR N-PSDB; ABL10212.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 25119; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB116176-AB110511), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins (AB55737-
 CC AB572072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pcr_sequences
 XX
 SQ Sequence 122 AA;
 Alignment Scores:
 Pred. No.: 2.07e-40 Length: 122
 Score: 400.50 Matches: 70
 Percent Similarity: 77.57% Conservative: 13
 Best Local Similarity: 65.42% Mismatches: 19
 Query Match: 41.63% Indels: 5
 DB: 4 Gaps: 2
 US-09-914-324a-3 (1-508) X ABB6109 (1-122)

QY 19 ATGATGTGATATCCCGAGCGGACACACAGAGCGC-----GCGGCAAGAG 66
 Db 16 MetAspPheAsnHisProIleGluIleProSerCysSerGlyGlyAlaValGlnAlaArgThrGlu 35
 QY 67 CGCTTTGAACTGAAAAAGTGAATGACATGACCTCTGCGCTGGGATATTGTGTTGAT 126
 Db 36 ArgPheValValIleValThrValAlaHisAlaMetTrpGlyTyrAspValAlaValAsp 55
 QY 127 AACTGTGCCATCTGCAGAACACCAATTATGATCTTTGATGAATGTCAAGCTAACCGAG 186
 Db 56 AsnCysAlaIleCysArgAsnHisIleMetAsnLeuGylleGluCysGlnAlaAsp--- 74
 QY 187 GCGTCCGCTACTTCAAAAGAGTGTACTGTGCGATGGGAGTGTCAACAGCTTTTAC 246
 Db 75 ProAsnAlaAsnGlnMetProGluCysThrValAlaTrpGlyGluCysAsnHisAlaPheHis 94
 QY 247 TTCACATGCACTCTGCTGCTGCTCAAAACACAGAGTGTGCTCATTTGACACAGAGAG 306
 Db 95 TyrHisCysIleLeuAlaArgTrpLeuValThrArgLeuValCysProLeuAspAsnGlyGlu 114
 QY 307 TGGGAATTCCTCAAAAGATAGG 327
 Db 115 TrpValTyrGlnIleValTyrGly 121
 RESULT 11
 AAB0814
 ID AAB0814 standard; protein; 121 AA.
 AC AAB0814;
 XX
 DT 02-JAN-2001 (first entry)
 DE A yeast cullin-interacting RING-H2 finger protein (Rbx1).
 XX
 KW Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;
 KW tumor suppressor; carcinoma; Ring box associated carcinoma;
 KW von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;
 KW cerebellar hemangioblastoma; hemangioma; retinal angioma;
 KM pheochromocytomas.
 XX
 OS Saccharomyces cerevisiae.
 XX
 FN WO200050445-A1.
 XX
 PD 31-AUG-2000.
 XX
 PF 25-FEB-2000; 2000WC-US004838.
 XX
 PF 26-FEB-1999; 99US-0121787P.
 XX
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 XX
 PI Conway JA, Conway RC, Kamura T;
 XX
 DR MPI; 2000-572067/53.
 XX
 DR N-PSDB; AAA74979.
 XX
 PT Cullin interacting RING-H2 finger protein, a component of von Hippel-
 PT Lindau tumor suppressor complex and Skp1-Cdc53p-F-box protein (SCF)
 PT ubiquitin ligase, useful for diagnosing and treating Ring box protein
 PT associated carcinomas.
 XX
 PS Disclosure; Page 34-35; 37pp; English.
 XX
 CC The present sequence represents a yeast cullin-interacting RING-H2 finger
 CC protein (Ring box protein), designated Rbx1. The human Rbx1 polypeptide
 CC is a tumor suppressor. Human Rbx1 is useful for diagnosing a
 CC predisposition of a patient to certain carcinomas. It is also useful for
 CC treating Ring box protein associated carcinomas or augmenting
 CC metabolically deficient system in animals. Human Rbx1 is also useful for
 CC evaluating the effectiveness of a therapeutic treatment for Ring box
 CC associated carcinomas. Human Rbx1 can be used to screen for agents which

XX 31-MAR-2000; 2000WO-US008621.
PF
XX
31-MAR-1999; 99US-0127607P.
PR
02-APR-1999; 99US-0127636P.
PR
05-APR-1999; 99US-0127728P.
PR
30-MAR-2000; 2000US-0054076P.
XX
XX (CMM) : CMMEXP CORR

PI Shimkets RA, Leach M;
XX
DR WPI; 2000-602362/57.
DR N-PSDB; AAC75216.
XX
XX Novel nucleic acids and peptides derived from open reading frame X,
PT

PT neurodegenerative disorders and cardiovascular disease.

PS Claim 11; Page 1266; 5507pp; English.
yy

CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC

CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
CC antinoriatic; antiarkinsonian; nootropic; neuroprotective; osteopathi;
CC

CC cardiatic; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;

CC dermatological; immunosuppressive; antihistaminic; antidiabetic; antiviral; antirheumatic; antithyroid; and antianaemic. The

sequences can be used to determine the presence or absence of a specific sequence. This is done by comparing the sequence of the sample to the sequence of the probe. If the sequences are identical, the probe will bind to the sample. If the sequences are different, the probe will not bind. This method is used to identify specific sequences in a sample.

proteins in gene therapy vectors. The proteins and nucleic acids may be

CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,

CC storage, systemic lupus erythematosus, severe combined immunodeficiency

disorders, asthma, allergic anaemia, burns, wounds, bone and joint diseases, bacterial haemoglobinuria, anti-inflammatory diseases, toxic

CC enhance coagulation; to inhibit thrombosis; and as a contraceptive

5Q Sequence 57 AA;

Alignment Scores: 6.6e-31
Pred. No.: 57
Length: 57

Score:	323.00	Matches:	55
Percent Similarity:	100.00%	Conservative:	0

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Best Local Similarity: 100.00% mismatches: 0
Query Match: 33.58% indels: 0
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5
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 12

 13

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L

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Y
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A
A
C

T
U
S

100

[illegible][illegible]

43 CysProLeuAsnAsnArg1uTrnG1uPheG1uIleTyrG1uHis 57

RESULT 13

AAU15873 standard: protein: 118 AA.
ID AAU15873

AA
AC AAU15873;

DT 07-NOV-2001 (first entry)

XX DE Human novel secreted protein, Seq ID 826.
XX KM Human; immunosuppressive; antiarthritic; antineumatic; cyrostatic;
XX KM cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
XX KM antibacterial; virucide; fungicide; ophthalmologic; vulnery;
XX KM secreted protein; rheumatoid arthritis; hyperproliferative disorder;
XX KM cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
XX KM cerebral ischaemia; angiogenesis; nervous system disorder;
XX KM Alzheimer's disease; infection; ocular disorder; corneal infection;
XX KM wound healing; epithelial cell proliferation; skin ageing; food additive;
XX KM preservative; antiproliferative.
XX OS Homo sapiens.
XX PN WO20015322-A2.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US001341.
XX PR 31-JAN-2000; 2000US-0179065P.
XX PR 04-FEB-2000; 2000US-0180628P.
XX PR 24-FEB-2000; 2000US-0184664P.
XX PR 02-MAR-2000; 2000US-0186350P.
XX PR 16-MAR-2000; 2000US-0189874P.
XX PR 17-MAR-2000; 2000US-0190076P.
XX PR 18-APR-2000; 2000US-0198123P.
XX PR 19-MAY-2000; 2000US-0205515P.
XX PR 07-JUN-2000; 2000US-0209467P.
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XX PR 26-JUL-2000; 2000US-0220964P.
XX PR 14-AUG-2000; 2000US-0224518P.
XX PR 14-AUG-2000; 2000US-0224519P.
XX PR 14-AUG-2000; 2000US-0225213P.
XX PR 14-AUG-2000; 2000US-0225214P.
XX PR 14-AUG-2000; 2000US-0225266P.
XX PR 14-AUG-2000; 2000US-0225267P.
XX PR 14-AUG-2000; 2000US-0225268P.
XX PR 14-AUG-2000; 2000US-0225270P.
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XX PR 06-SEP-2000; 2000US-0230437P.
XX PR 08-SEP-2000; 2000US-0231242P.
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XX PR 08-SEP-2000; 2000US-0233081P.
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PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234224P.
PR 25-SEP-2000; 2000US-0234987P.
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PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236337P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
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PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
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PR 08-NOV-2000; 2000US-0246536P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
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PR 17-NOV-2000; 2000US-0249213P.
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PR 17-NOV-2000; 2000US-0249216P.
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PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249255P.
PR 17-NOV-2000; 2000US-0249257P.
PR 17-NOV-2000; 2000US-0249259P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.

GenCore version 5.1.6
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OW nucleic - protein search, using frame_plus_n2p model

Run on: March 25, 2004, 09:19:21 ; Search time 20 Seconds
(without alignments)
2622.599 Million cell updates/sec

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Perfect score: 962
Sequence: 1 ccccaaatgagcgagcgat.....aaagtcagtcgattccgg 508

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues
Total number of hits satisfying chosen parameters: 778828

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-NO_MMAP -IARGOUTRY -NEG_SCORES=0 -WAIT -DSBLOCAT=100 -LONGLOC
-DEV_TIMEOUT=120 -MAXN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	208	20.6	84	US-09-599-360B-77	Sequence 77, Appl
2	194.5	20.2	112	US-09-621-976-5805	Sequence 5605, Ap
3	193.5	20.1	112	US-09-621-976-5677	Sequence 5677, Ap
4	105.5	11.0	94	US-09-621-976-5714	Sequence 5714, Ap
5	85	8.8	104	US-09-325-932A-49	Sequence 49, Appl
6	85	8.8	664	US-09-268-140-2	Sequence 2, Appl
7	83	8.6	337	US-09-828-303-18	Sequence 18, Appl
8	81	8.8	273	US-09-252-991A-22218	Sequence 22218, A
9	80	8.3	180	US-08-786-606-3	Sequence 3, Appl
10	80	8.3	180	US-08-933-750C-48	Sequence 48, Appl
11	80	8.3	180	US-09-234-613-48	Sequence 48, Appl
12	80	8.3	284	US-08-786-606-9	Sequence 9, Appl

13	79	8.2	50	US-09-052-089A-15	Sequence 15, Appl
14	79	8.2	359	US-09-663-600A-106	Sequence 106, App
15	79	8.2	381	US-08-867-057-1	Sequence 1, Appl
16	79	8.2	381	US-08-867-057-3	Sequence 3, Appl
17	79	8.2	381	US-09-128-369-1	Sequence 1, Appl
18	79	8.2	381	US-09-128-369-3	Sequence 3, Appl
19	79	8.2	381	US-09-663-600A-200	Sequence 200, App
20	79	8.2	410	US-07-945-283-4	Sequence 4, Appl
21	77.5	8.1	1493	US-09-423-890-8	Sequence 8, Appl
22	77.5	8.1	1593	US-08-628-829-4	Sequence 4, Appl
23	76.5	8.0	317	US-09-921-099A-8	Sequence 8, Appl
24	76.5	8.0	1302	US-09-423-890-2	Sequence 2, Appl
25	75.5	7.8	305	US-09-599-360B-114	Sequence 114, Appl
26	75	8.1	555	US-09-252-991A-24056	Sequence 24056, A
27	74.5	7.7	67	US-07-945-283-5	Sequence 5, Appl
28	74.5	7.7	149	US-09-690-454-205	Sequence 205, App
29	74.5	7.7	166	US-09-690-454-204	Sequence 204, App
30	74.5	8.1	392	US-09-328-352-6498	Sequence 6498, Ap
31	74.5	7.7	826	US-09-894-998A-47	Sequence 47, Appl
32	74	8.0	144	US-09-252-991A-25847	Sequence 25847, A
33	74	7.7	327	US-09-290-640-66	Sequence 66, Appl
34	74	7.7	327	US-09-665-615B-66	Sequence 66, Appl
35	73	7.9	436	US-09-328-352-4416	Sequence 4416, Ap
36	73	7.6	542	US-09-449-632-4	Sequence 4, Appl
37	73	7.6	551	US-08-699-103B-25	Sequence 25, Appl
38	73	7.6	551	US-09-229-059-25	Sequence 25, Appl
39	73	7.6	551	US-09-628-133-25	Sequence 25, Appl
40	72.5	7.5	66	US-09-205-258-1030	Sequence 1030, Ap
41	72.5	7.5	69	US-07-945-283-6	Sequence 6, Appl
42	72.5	7.5	84	US-09-205-258-1032	Sequence 1032, Ap
43	72.5	7.5	167	US-09-205-258-1026	Sequence 1026, Ap
44	72.5	7.5	276	US-08-786-606-5	Sequence 5, Appl
45	72.5	7.5	276	US-09-205-258-1027	Sequence 1027, Ap

ALIGNMENTS

RESULT 1
US-09-599-360B-77
Sequence 77, Application US/09599360B
Patent No. 6548633
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Bouguerelet, L.
APPLICANT: Jobert, S.
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: GENSET.050CP3
CURRENT APPLICATION NUMBER: US/09/599,360B
CURRENT FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/469,099
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patent.pm
SEQ ID NO 77
LENGTH: 84
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-599-360B-77
Alignment Scores:
Pred. No.: 5.4e-17
Score: 208.00
Percent Similarity: 56.82%
Best Local Similarity: 37.50%
Query Match: 21.62%
DB: 4
Gaps: 2
US-09-914-324A-3 (1-508) x US-09-599-360B-77 (1-84)


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; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5714
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -53..-1
; NAME/KEY: UNSURE
; LOCATION: 14
; OTHER INFORMATION: Xaa = Glu,Gln
US-09-621-976-5714

Alignment Scores:
Pred. No.: 0.000198 Length: 94
Score: 105.50 Matches: 15
Percent Similarity: 56.10% Conservative: 8
Best Local Similarity: 36.59% Mismatches: 13
Query Match: 10.97% Indels: 5
DB: 4 Gaps: 1

US-09-914-324A-3 (1-508) x US-09-621-976-5714 (1-94)

QY 148 CACATTATGATCTTTGCAATGATGCAAGCTAACAGGCGCCGCTACTTCAGAGAG 207
DB 10 HistHthrspAlaAlaProAspCysLys-----ValProGlyAspAsp 24
QY 208 TGTACTGTGCGATGGAGGTCTGTAAACCATGCTTTTCACCTTCGATGCTCTGCTGG 267
DB 25 CysProLeuValTrpGlyGlnCysSerHisCysPheHisMetHisCysIleLeuLysTrp 44
QY 268 CTC 270
DB 45 Leu 45

RESULT 5
US-09-325-932A-49
; Sequence 49, Application US/09325932A
; Patent No. 6451504
; GENERAL INFORMATION:
; APPLICANT: Film, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325, 932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-325-932A-49

Alignment Scores:
Pred. No.: 0.0665 Length: 104
Score: 85.00 Matches: 20
Percent Similarity: 39.47% Conservative: 10
Best Local Similarity: 26.32% Mismatches: 32
Query Match: 8.84% Indels: 14
DB: 4 Gaps: 1

US-09-914-324A-3 (1-508) x US-09-325-932A-49 (1-104)

QY 130 TGTGCAATCTGACAGAACACATTATGATCTTTGCAATGATGCAAGCTAACAGGCG 189
DB 25 CysAlaValCysLeuSerLysPheGluAspLys----- 35
QY 190 TCCGCTACTTGAAGAGTGTACTGTCCATGAGGAGTCTGTAAACCATGCTTTTCACCTC 249
DB 36 -----GluIleLeuArgPheLeuProLysCysArgHisAlaPheHisIle 50
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QY 250 CACTGCATCTCTGCTGCTGCTCAAAAACAGCAGGATGTGTCCATTGACACAGAGATGG 309
DB 51 AspCysIleAspTrpTrpLeuGlnLysHisSerSerCysProLeuCysArgHisLysVal 70
QY 310 GAATTCCAAAAGTATGAGCACTAGAAAAGACTCTTCCATCCATGAGCTT 357
DB 71 SerAlaGluAspProAlaAsnPheThrTyrThrAsnSerMetArgLeu 86

RESULT 6
US-09-268-140-2
; Sequence 2, Application US/09268140
; Patent No. 6268176
; GENERAL INFORMATION:
; APPLICANT: Gemmill, Robert M.
; APPLICANT: Drabkin, Harry A.
; TITLE OF INVENTION: TRC9, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED
; FILE REFERENCE: 93445-00004
; CURRENT APPLICATION NUMBER: US/09/268, 140
; CURRENT FILING DATE: 2000-03-12
; PRIOR APPLICATION NUMBER: US 60/077, 723
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 664
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-268-140-2

Alignment Scores:
Pred. No.: 0.129 Length: 664
Score: 85.00 Matches: 24
Percent Similarity: 40.48% Conservative: 10
Best Local Similarity: 28.57% Mismatches: 22
Query Match: 8.84% Indels: 28
DB: 3 Gaps: 4

US-09-914-324A-3 (1-508) x US-09-268-140-2 (1-664)

QY 64 AAGCGCTTGAAGTAAAGTGAATGACAGAGCCCTGTGGCGGATATT----- 117
DB 522 ArgArgThrAlaValLysLysLysLeuPro-----GluIleLysGly 537
QY 118 -----GTGGTGTATGACTGTGCATCTTCAGAGACCATTAATGATCTT 162
DB 538 SerArgLeuGlnGluLysAlaAspValCysAlaIleCysTyrHisGluPhe----- 554
QY 163 TGCATAGATGTCAAGCTAACAGGCGCCGCTACTTCAGAAAGTGTACTGTGCATGG 222
DB 555 -----ThrThrSerAlaArgIleThr----- 561
QY 223 GGAGTGTAAACCATGCTTTTCACCTTCACGATGCTCTGCTGCTCAAAACAGCAGAG 282
DB 562 ---ProCysAsnHisTyrPheHisAlaLeuCysLeuArgLysTrpLeuTyrIleGlnAsp 580
QY 283 GTGTGTCATTG 294
DB 581 ThrCysProMet 584

RESULT 7
US-09-828-303-18
; Sequence 18, Application US/09828303
; Patent No. 6677504
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: BOHNETT, HANS J.
; APPLICANT: VAN THIELEN, MOCHA
; APPLICANT: CHEN, ROUYING
; TITLE OF INVENTION: TRANSCRIPTION FACTOR STRESS-RELATED PROTEINS AND
; FILE REFERENCE: 16313-0030
; CURRENT APPLICATION NUMBER: US/09/828, 303
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/ CURRENT FILING DATE: 2001-08-20
/ PRIOR APPLICATION NUMBER: 60/196,001
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 79
/ SOFTWARE: Patent Ver. 2.1
/ SEQ ID NO 18
/ LENGTH: 337
/ TYPE: PRF
/ ORGANISM: Physcomitrella patens
US-09-828-303-18

Alignment Scores:
Pred. No.: 0.178 Length: 337
Score: 83.00 Matches: 17
Percent Similarity: 41.38% Conservative: 7
Best Local Similarity: 29.31% Mismatches: 20
Query Match: 8.63% Indels: 14
DB: 4 Gaps: 2

US-09-914-324A-3 (1-508) x US-09-828-303-18 (1-337)

QY 121 GTTGATTAAGTGGCCATCTGACGAGAACCATTAATGATCTTTGCATGAATGTCAGCT 180
DB 85 ValPheGluCysAlaValCysLeuGlu-----GluPheGluLeu 97
QY 181 AACGAGCGCTCCGCTCTTCAGAGAGTGTACTGTGCATGGGAGTGTGTACCATGCT 240
DB 98 GlyAluLysGlyAlaGhrThrLeuProLys-----CysAspHisSer 110
QY 241 TTTCATCTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 294
DB 111 PheHisLeuAspCysThrLeuAspMetTrpLeuHisSerHisSerThrCysProLeu 128

RESULT 8
US-09-252-991A-22218
/ Sequence 22218, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfeld et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 22218
/ LENGTH: 273
/ TYPE: PRF
/ ORGANISM: Pseudomonas aeruginosa
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: (180)
/ OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-22218

Alignment Scores:
Pred. No.: 0.29 Length: 273
Score: 81.00 Matches: 31
Percent Similarity: 34.51% Conservative: 8
Best Local Similarity: 27.43% Mismatches: 54
Query Match: 8.79% Indels: 20
DB: 4 Gaps: 4

US-09-914-324A-3 (1-508) x US-09-252-991A-22218 (1-273)

QY 349 TGAAGAAGCTTTTCTAGTACGACATCTTGGCATTCGATCCATCTGTTGTGCA---.293
DB 13 ThrThrCysCysValProCysArgArgSerArgGlyCysSerThrArgCysSerProGln 32

QY 292 -----ATGACACACCTGTGCTGTTTGAAGCAGGAGAGATGACGTGGAAGT 245
DB 33 TrpAlaThrAlaSerLeuThrProVal-----SerProArgThrSerAlaThr 48
QY 244 GAAAGCATGTTTACAGACTCCCATGACGACAGTACACTCTTGTGAGTAGGAGCGCT 185
DB 49 SerArgArgAlaSerProThrProThrSerSerThr-----AlaPro 63
QY 184 GGTTAAGTACATTTATGACAAAGATCCATATATGCTTCTTCGACATGACAGCTTAT 125
DB 64 AlaSerSerProArgThrTrpArgSerProCysArgProSerCysCysTrpLysProAla 83
QY 124 CAACCAATATATCCAGCCGAGAGGAGGCTACTG-----CATTCACCT 83
DB 84 ThrProArgCysProThrProThrProSerSerAlaValAlaTrpGlyThrAlaGlyLysSerThr 103
QY 82 TTTCATCTCAAGCGCTTCTTGCCTCCGCGCGCTGTGG 44
DB 104 AlaProSerArgAlaAlaSerArgSerArgArgCysTrp 116

RESULT 9
US-08-786-606-3
/ Sequence 3, Application US/08786606
/ Patent No. 5861495
/ GENERAL INFORMATION:
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Au-Young, Janice
/ APPLICANT: Coleman, Roger
/ APPLICANT: Goli, Surya K.
/ TITLE OF INVENTION: NOVEL HUMAN ZINC-BINDING
/ TITLE OF INVENTION: PROTEINS
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,606
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy R
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0173 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-786-606-3

Alignment Scores:
Pred. No.: 0.331 Length: 180
Score: 80.00 Matches: 29
Percent Similarity: 39.81% Conservative: 12
Best Local Similarity: 28.16% Mismatches: 18
Query Match: 8.32% Indels: 44

Thu Mar 25 10:42:34 2004

us-09-914-324a-3.rai

Page 7

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CORRESPONDENCE ADDRESS:
ADDRESSER: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,089A
FILING DATE: 31-Mar-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-198 CIP 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-052-089A-15

Alignment Scores:
Pred. No.: 0.278 Length: 50
Score: 79.00 Matches: 17
Percent Similarity: 46.55% Conservative: 10
Best Local Similarity: 29.31% Mismatches: 15
Query Match: 8.21% Indels: 16
Gaps: 3

US-09-914-324A-3 (1-508) X US-09-052-089A-15 (1-50)

QY 124 GATPACTGTCGCATCTTGACAGAAACACATTATGATCTTTGCATAGAAATGTCAGCTAAC 185
Db 2 AspaValcysAlaIleIcysLeuAapGluTyrGluAsp----- 13
QY 184 CAGGCGTCGCTACTTCAGAGAGATGATCTGTCGATGGGAGACTGTGAACATGCTTTT 244
Db 14 -----GlyAspIysLeuAAGIleLeu-----ProCysSerHisAlaTyr 26
QY 244 CACTTCACATGCATCTCTCTGCTGGCTC---AAAACAGACAGAGTGTGTCATTG 294
Db 27 HiscysIysCysValasPprrTiplleuThrIysThrIysIysThrCysAcprrval 44

RESULT 14
US-09-663-600A-106
Sequence 106, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duguet, Aymeric
APPLICANT: Bouguetier, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A
PRIOR APPLICATION NUMBER: 09/151,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677

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PRIORITY FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60//069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60//074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60//081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60//096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60//099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 106
LENGTH: 359
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -34..-1
NAME/KEY: UNSURE
LOCATION: 20,64,65,130,156,282,288,289,294,296,300,302,310
OTHER INFORMATION: Xaa = any one of the twenty amino acids
US-09-663-600A-106

Alignment Scores:
Pred. No.:      0.562      Length:      359
Percent:        79.00     Matches:      17
Score Similarity: 46.55%    Conservative: 10
Best Local Similarity: 29.31% Mismatches:   15
Query Match:      8.21%     Indels:       16
DB:               Gaps:      3

US-09-914-324A-3 (1-508) x US-09-663-600A-106 (1-359)

CY 124 GATTAACGTGTCATCTGCAGAACACCATATMGATCTTGCATAGATGCAAGCTAAC 183
    ||| ||||| ||||| ||| :||
DB 238 AspvAlCysAlAlIleCysIeuAspDlurYrGlunsp-----249
CY 184 CAGGCGTCGGCTACTTCCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACATGCTTT 243
    :||||| :||||| :||| :|||
DB 250 -----GIyAspIyeuArgIleuu-----ProCySerHisAlatyr 263
CY 244 CATTCGACGTGATCTCTGCGTGCTC---AAAACAGCAGCAGGTGTGCCATTG 294
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 263 HisCylsCysValAspProtIreuthrlyshYsrlysthrYCysproval 280

RESULT 15
US-08-667-057-1
Sequence 1, Application US/0867057
Patent No. 5840535
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: NEW ZINC RING PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,057
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:

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APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy U.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0311 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-885-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 381 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: EMAROT02
 CLONE: 104119
 US-08-867-057-1

Alignment Scores:
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 Score: 79.00 Matches: 17
 Percent Similarity: 46.55% Conservative: 10
 Best Local Similarity: 29.31% Mismatches: 15
 Query Match: 8.21% Indels: 16
 DB: 2 Gaps: 3

US-09-914-324A-3 (1-508) x US-08-867-057-1 (1-381)

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 DB 238 AspValCysAlaIleCysLeuAspGluTyrGluAsp----- 249
 QY 184 CAGGCGTCGCTACTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTACCATGCTTT 243
 DB 250 -----GlyAspIleuArgIleLeu-----ProCysSerHisAlaTyr 262
 QY 244 CACTTCACATGATCTCTCGCTGCTC---AAACAGCAGCAGGTGTGCATG 294
 DB 263 HisCysLysCysValAspProTyrLeuThrLysIleLysTyrCysProVal 280

Search completed: March 25, 2004, 09:25:16
 Job time : 23 secs

Thu Mar 25 10:42:34 2004

us-09-914-324a-3.rapb

Page 1

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_r2p model

Run on: March 25, 2004, 09:23:42 ; Search time 42.5 Seconds
(without alignments)
6255.256 Million cell updates/sec

Title: US-09-914-324a-3

Perfect score: 962

Sequence: 1 cccaatgctgcgcagcgat.....aaagtcacgttgatctctg 508

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Zgapop 6.0, Zgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1065169 segs, 261661801 residues

Total number of hits satisfying chosen parameters: 2130338

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Blomum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=plc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USPR=US09913324 @CGN 1.1.13 @runac_25032004_090849_8856
-NCPU=6 -ICPU=3 -NO MMAP -LARGEBUFFER -NEG_SCORES=0 -WAIT -DSPLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Database : Published Applications AA:

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result Query SUMMARIES
No. Score Match Length DB ID Description

1	616	64.0	108	9	US-09-826-312-6	Sequence 6, Appli
2	616	64.0	108	14	US-10-108-767-6	Sequence 6, Appli
3	616	64.0	108	14	US-10-152-156-6	Sequence 6, Appli
4	518.5	52.9	118	12	US-10-424-599-148916	Sequence 148916,
5	506.5	52.9	152	12	US-10-424-599-221431	Sequence 221431,
6	420.5	43.7	106	12	US-10-424-599-148915	Sequence 148915,
7	420.5	43.7	106	12	US-10-424-599-230014	Sequence 230014,
8	234	30.6	118	9	US-09-764-864-8826	Sequence 826, App
9	232	30.4	131	9	US-09-764-864-1285	Sequence 1285, App
10	287	29.8	64	12	US-10-424-599-253520	Sequence 228320,
11	287	29.8	113	9	US-09-826-312-8	Sequence 8, Appli
12	287	29.8	113	14	US-10-108-767-8	Sequence 8, Appli
13	287	29.8	113	14	US-10-152-156-8	Sequence 8, Appli
14	282	29.3	68	12	US-10-424-599-242288	Sequence 242288,
15	282	29.3	68	12	US-10-424-599-264079	Sequence 264079,
16	214.5	22.3	40	12	US-09-764-864-1284	Sequence 1284, Ap
17	213	22.1	88	12	US-10-276-774-2678	Sequence 2678, Ap
18	213	22.1	88	14	US-10-102-806-620	Sequence 620, App
19	213	22.1	91	15	US-10-264-049-2937	Sequence 2937, App
20	213	22.1	105	9	US-09-764-864-1274	Sequence 1274, Ap
21	208	21.6	84	12	US-10-221-625-94	Sequence 94, Appl
22	208	21.6	100	12	US-10-424-599-251860	Sequence 251860,
23	202.5	21.0	85	15	US-10-264-049-2926	Sequence 2926, Ap
24	202	21.0	84	14	US-09-826-312-5	Sequence 5, Appli
25	202	21.0	84	14	US-10-108-767-5	Sequence 5, Appli
26	202	21.0	84	14	US-10-152-156-5	Sequence 5, Appli
27	186.5	19.4	121	9	US-09-764-864-839	Sequence 839, App
28	186.5	19.4	121	9	US-09-764-864-1294	Sequence 1294, Ap
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30	175.5	18.2	114	15	US-10-320-797-3003	Sequence 3003, Ap
31	175	18.2	73	12	US-10-424-599-235108	Sequence 235108,
32	164	17.0	124	12	US-10-425-114-37253	Sequence 37253, A
33	138	14.3	34	12	US-10-424-599-254645	Sequence 254645,
34	135.5	14.1	133	14	US-10-032-585-7259	Sequence 7259, Ap
35	102	10.6	144	12	US-10-424-599-279773	Sequence 279773,
36	100.5	10.4	205	12	US-10-424-599-213911	Sequence 213911,
37	98	10.1	234	12	US-10-424-599-26133	Sequence 26133,
38	97.5	10.1	128	12	US-10-424-599-202919	Sequence 202919,
39	97.5	10.1	194	12	US-10-424-599-202919	Sequence 202919,
40	97.5	10.1	195	12	US-10-425-114-36967	Sequence 36967, A
41	97.5	10.1	209	12	US-10-425-114-41999	Sequence 41999, A
42	97.5	10.1	209	12	US-10-425-114-61173	Sequence 61173, A
43	96.5	10.0	345	12	US-10-425-114-71489	Sequence 71489, A
44	96.5	10.0	356	12	US-10-424-599-179820	Sequence 179820,
45	96.5	10.0	357	12	US-10-424-599-267968	Sequence 267968,

ALIGNMENTS

RESULT 1
US-09-826-312-6
Sequence 6, Application US/09826312
Patent No. US20020042083A1
GENERAL INFORMATION:
APPLICANT: Isekan, Sarkiz D.
APPLICANT: Huang, Jianting
APPLICANT: Sheng, Julie
APPLICANT: Pray, Todd R.
TITLE OF INVENTION: UBIQUITIN LIGASE ASSAY
FILE REFERENCE: A-68613-1/RMS/JTD
CURRENT APPLICATION NUMBER: US/09/826,312
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 09/542,497
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patent version 3.1
SEQ ID NO 6
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
US-09-826-312-6
Alignment Scores:

QY 265 TGGCTCAAAACACAGAGGTGTTCATTGCAACAGAGTGGAAATTCAAAAGTAT 324
DB 97 TTPVallysGlnAsnAsnArgCysProLeuGlnAsnTPValValGlnArgGile 116
QY 325 GGG 327
DB 117 Gily 117

RESULT 9
US-09-764-864-1285
; Sequence 1285, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO: 1285
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (11)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1285

Alignment Scores:
Pred. No.: 2,15e-24 Length: 131
Score: 292.00 Matches: 49
Percent Similarity: 64.95% Conservative: 14
Best Local Similarity: 50.52% Mismatches: 30
Query Match: 30.35% Indels: 4
DB: Gaps: 2

US-09-914-324A-3 (1-508) x US-09-764-864-1285 (1-131)

QY 37 AGCGGACCAACAGCGCGCGGCAAGAGCGCTTGAAGTGAAGTGAAGTACAGTA 96
DB 38 SerGlySerLysSerGly---GlyAspLysMetPheSerLeuLysLysTriPhsnAlaVal 56
QY 97 GCCCTCTGGCCCTGGGATATGTGTGATTAACCTGTGCCATCTGCAGGAACCACTATAG 156
DB 57 AlameetripserTripsrValGlnCysAspThrCysAlaIleCysArgValGlnValmet 76
QY 157 GATCTTTGATAGATGTCAGCTAACCAAGCGCTCCGCTACTTCAGAGAGTGTACTGTC 216
DB 77 AspAlaCysLeuArgCysGlnAlaGluAsn-----LysGlnGlnAspCysValVal 93
QY 217 GATGGGAGGTCTGTACCACTGTTTTCACCTTCCACTGCATCTCTCGCTGGCTCAAAACA 276
DB 94 ValTriPcilyGlnCysAsnHisSerPheHisAsnCysCysMetSerLeuTriValysGln 113
QY 277 CGACAGGTGTCTTCATTGCAACAGAGTGGAAATTCAAAAGTATAGG 327
DB 114 AsnAsnArgCysProLeuGlnAsnTPValValGlnArgGile 130

RESULT 10
US-10-424-599-238320
; Sequence 238320, Application US/10424599
; Patent No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILER REFERENCE: 38-21(53223)B

QY 139 TGCAGAACCACTATATGATCTTTGCTATGATGTCAGTCAAGCTAACAGCGCTCCGCTACT 198
DB 1 CysArgAsnHisLeuMetGlyPheCysIleGlnGlnAlaAsnGlnGlyArgAlaPro 20
QY 199 TCAGAAAGTGTACTGTCCGATGCGAGGAGTCTGTAACTTCTTTCACTTCCACTGCATC 258
DB 21 AsnGlnGlnCysProValAlaTriGlyValCysAsnHisAlaPheSerPheProCysIle 40
QY 259 TCTCGCTGGCTCAAAACAGAGAGTGTGTCCCTTGGACACAGAGAGTGGAAATTCCAA 318
DB 41 SerArgTriPallysThrArgGlnValCysProLeuAspAsnSerLysTriPglyPheGln 60
QY 319 AAGTATGGG 327
DB 61 LysTriGly 63

RESULT 11
US-09-826-312-8
; Sequence 8, Application US/09826312
; Patent No. US20020042083A1
; GENERAL INFORMATION:
; APPLICANT: Isaakani, Sarkiz D.
; APPLICANT: Huang, Julie
; APPLICANT: Sheung, Julie
; TITLE OF INVENTION: UBIQUITIN LIGASE ASSAY
; FILE REFERENCE: A-68613-1/RMS/JJD
; CURRENT APPLICATION NUMBER: US/09/826,312
; CURRENT FILING DATE: 2001-04-03
; Prior application number: US 09/542,497
; Prior filing date: 2000-04-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent version 3.1
; SEQ ID NO: 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-312-8

Alignment Scores:
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Score: 287.00 Matches: 48
Percent Similarity: 63.92% Conservative: 14
Best Local Similarity: 49.48% Mismatches: 31
Query Match: 29.83% Indels: 4
DB: Gaps: 2

US-09-914-324A-3 (1-508) x US-09-826-312-8 (1-113)

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Db 41 AsnCySAIAlIeCysArGAsnHisIleMetAspLeuCyAlIeGluCysGlnAlaAsnGln 60
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 Db 61 AlAsrAlaIatHserSerGluGluCysThrValAlaIatpGlyValCysAsnHisAlaPheHis 80
 QY 247 TTCACATGCATCTCTCGTGGCTCACAACACGACAGGTGTTCCTATGGACAAACAGAG 306
 Db 81 PheHisCysIleSerArGTrpLeuYstHrArgInValCysProLeuAspAsnArgGln 100
 QY 307 TGGGAATTCCAAAGATGGGCAC 330
 Db 101 TrpGluPheGlnIlystYrGlyHis 108

RESULT 2

T13388
 hypothetical protein T13388.11 - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
 C:Accession: T13388
 R:Salles, C.; Valenti, P.; Dartamitsu, A.; Henderson, N.; Campbell, L.; Glover, D.
 Submitted to the EMBL Data Library, May 1999
 A:Description: Sequencing the discal X chromosome of Drosophila melanogaster.
 A:Reference number: Z17665
 A:Accession: T13388
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-136 <CAT>
 A:Cross-references: EMBL:AL031581, PIDN:CAA20888.1
 C:Genetics:
 A:Cross-references: Flybase:FBgn0020381
 A:Introns: 64/1
 A>Note: EG:115C2.11

Alignment Scores:
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US-09-914-324a-3 (1-508) x T13388 (1-136)

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 QY 64 AAGGGCTTGAAGGAAAG-----84
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 QY 85 -----TGGAAATGCAGTACC 99
 Db 40 CysThrAspGlyAsnThrSerSerPheProLeuArGArgLysGlnItrPAsnAlaValAla 59
 QY 100 CTCTGGGCGCTGGATATTGGTGTGATGATGCTGCATGTCAGAGAACCATATGAT 159
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 QY 160 CTTCGATAGATGTCAAGCTAACCGGCGTCCGCTACTTCAAGAGGTGACTGTGCA 219
 Db 80 LeuCySileGluCysGlnAlaAsnGlnIAsrAlaThrSerGluGluCysThrValAla 99
 QY 220 TGGGAGTCTGTAAACCATGCTTTTCATCTTCAGATGATCTCCCTGGCTCAAAACAGA 279
 Db 100 TrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArGTrpLeuYstHrArg 119
 QY 280 CAGGTGTGCTCATTTGACAAACAGAGAGTGGGAATTCCAAAGTATGGGCAC 330
 Db 120 GlnValCysProLeuAspAsnArgGluTrpAspPheGlnIlystYrGlyHis 136

RESULT 3

T47341
 ring-box protein-like - Arabidopsis thaliana
 N:Alternate names: Protein T21C14.50
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Aug-2002
 C:Accession: T47341
 R:Delserny, M.; Berger, C.; Cooke, R.; Gaubler, P.; Grellet, F.; Laudie, M.; Mewes, H.W.

Submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z24462
 A:Accession: T47341
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-115
 A:Cross-references: EMBL:AL138639
 A:Experimental source: cultivar Columbia; BAC clone T21C14
 C:Genetics:
 A:Map position: 3
 A:Introns: 43/1; 60/1; 80/1; 104/1
 A>Note: T21C14.50
 C:Superfamily: Yeast hypothetical protein YOL133w; RING finger homology

Alignment Scores:
 Pred. No.: 2.84e-46 Length: 115
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 Best Local Similarity: 81.48% Mismatches: 13
 Query Match: 51.87% Indels: 2
 DB: 2 Gaps: 1

US-09-914-324a-3 (1-508) x T47341 (1-115)

QY 7 ATGGCGGACGATGATGTGATATCCCGAGCGGCACCAACAGCGCGCGGCAAG 66
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 QY 67 CGCTTGAAGTGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 126
 Db 28 ArGpHeGluLeuLysLysTrpSerAlaValAlaLeuTrpAlaTrpAspIleValAla 47
 QY 127 AACTGTGCATCTCGAGAACCACTTATGATCTTTGATGATGATGATGATGATGAT 186
 Db 48 AsnCySAIAlIeCysArGAsnHisIleMetAspLeuCySileGluCysLeuAlaAsnGln 67
 QY 187 GCGTCGGCTACTTCAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 246
 Db 68 AlAsrAlaIatHserSerGluGluCysThrValAlaIatpGlyValCysAsnHisAlaPheHis 87
 QY 247 TTCACATGCATCTCTCGTGGCTCACAACACGACAGGTGTTCCTATGGACAAACAGAG 306
 Db 88 PheHisCysIleSerArGTrpLeuYstHrArgInValCysProLeuAspValCysGln 107
 QY 307 TGGGAATTCCAAAGATGGGCAC 330
 Db 108 TrpGluPheGlnIlystYrGlyHis 115

RESULT 4

T27823
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 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T27823
 R:McMurray, A.
 Submitted to the EMBL Data Library, April 1996
 A:Reference number: Z20425
 A:Accession: T27823
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-110 <WIL>
 A:Cross-references: EMBL:Z70757, PIDN:CAA94801.1, GSPDB:GN00023, CESP:ZK287.5
 A:Experimental source: clone ZK287
 C:Genetics:
 A:Gene: CESP:ZK287.5

A:Map position: 5
A:introns: 25/3; 94/3

Alignment Scores:

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		Gaps:	2

US-09-914-324A-3 (1-508) x T27823 (1-110)

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QY 7 ATGGCGGCGCGATGGAT-----GTGGATACCCGAGCGGACCAAGCGGCGG 57
DB 1 MetAlaGlnAlaSerAspSerThrAlaMetGluValGluGlnAlaThrAsnGlnThrVal 20
QY 58 GGCAGAGCGCGTTGAGTGAAGGATGAGATGAGCGCTGGGCGTGGATATT 117
DB 21 --LysLysArgPheGluValLysLysTyrSerAlaValAlaLeuTyrPalaTyrPspIle 39
QY 118 GTGTTGATTAAGTGGCATCTGCAGAACCAATTATGATCTTTGATGAATGTCAA 177
DB 40 GlnValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGln 59
QY 178 GCTAACCCAGGCGTCCGCTACTTCAGAGAGTACTGTGCGATGGGAGTCTGTAACTAT 237
DB 60 AlaAsnGlnAlaAlaGlyLeuLysAspGluCysThrValAlaTyrGlyAsnCysAsnHis 79
QY 238 GCTTTCACTTCATCTGCATCTCTGCGTGGCTCAAAACAGACGAGTGTGTCATTGGAC 297
DB 80 AlaPheHisPheHisCysIleSerArgTyrPheLysTyrThrArgGlnValCysPheLeuAsp 99
QY 298 AACAGAGTGGGAAATTCGAAATGATGGGCAC 330
DB 100 AsnArgGluTyrGluPheGlnLysTyrGlyHis 110

```

RESULT 5

POP-Interacting protein 1 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T38310
R:Brown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z21733
A:Accession: T38310
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-107 <BRO>
A:Cross-references: EMBL:Z98977; PIDN:CA85859.1; GSPDB:GN00066; SPDB:SPAC23H4.18c
A:Experimental source: strain 97zh-; cosmid c23H4
C:Genetics:
A:Gene: SPDB:SPAC23H4.18c
A:Map position: 1
A:introns: 25/3; 75/3; 106/1

Alignment Scores:

Pred. No.:	5.55e-43	Length:	107
Score:	469.00	Matches:	77
Percent Similarity:	92.05%	Conservative:	4
Best Local Similarity:	87.50%	Mismatches:	7
Query Match:	48.75%	Indels:	0
		Gaps:	0

US-09-914-324A-3 (1-508) x T38310 (1-107)

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QY 67 CGCTTGAAGTGAAGGATGAGTGAAGCGCTGGGCGTGGATTTGGTGTAT 126
DB 20 ArgPheGlnIleLysLysTyrPheAsnAlaValAlaLeuTyrGlnTyrPspIleValAlaAsp 39
QY 127 AACTGTGCATCTGCAGAACCAATTATGATCTTTGATGAATGTCAACCTAACGAG 186

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DB 40 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnThr 59
QY 187 GCGTCCGCTACTTCAGAGAGTGAAGTGAAGTGGAGTGTGAACCATGCTTTTCAC 246
DB 60 AspSerAlaAlaAlaGlnIleCysThrValAlaTyrPalaTyrPspIleValAlaPheHis 79
QY 247 TTCACATGCACTCTCTGCTGGCTCAAAACAGACAGGTGTTCATTGGACACAGAGG 306
DB 80 PheHisCysIleSerArgTyrPheAsnThrArgSerValCysPheLeuAspAsnArgGlu 99
QY 307 TGGAAATCCAAAGTATGGGCAC 330
DB 100 TyrGluPheGlnArgTyrGlyHis 107

```

RESULT 6

hypothetical protein YOL133w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein AOA1121; hypothetical protein O0511
C:Species: Saccharomyces cerevisiae
C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 02-Aug-2002
C:Accession: S66830; S72035
R:Arino, J.; Casamayor, A.; Gamo, F.J.; Gancedo, C.; Lafuente, M.J.; Aldea, M.; Casas, C.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66814
A:Accession: S66830
A:Molecule type: DNA
A:Residues: 1-121 <ARI>
A:Cross-references: EMBL:Z74876; NID:g1420022; PID:g1420024; MIPS:YOL133w
A:Experimental source: strain S288C
R:Aldea, M.; Piedrafitra, L.; Casas, C.; Casamayor, A.; Khalid, H.; Balcells, L.; Arino, J.
Yeast 12, 1053-1058, 1996
A:Title: Sequence analysis of a 12 801 bp fragment of the left arm of yeast chromosome X
protein and six other open reading frames.
A:Reference number: S72030; MIMD:s7051593; PMID:8896270
A:Accession: S72035
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-121 <ALD>
A:Cross-references: EMBL:X95465; NID:g1628437; PID:CA84737.1; PID:g1628443
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, DNA
C:Genetics:
A:Gene: SGD:HRT1
A:Cross-references: SGD:S0005493
A:Map position: 15L
A:Note: YOL133w
C:Superfamily: yeast hypothetical protein YOL133w; RING finger homology

Alignment Scores:

Pred. No.:	9.16e-34	Length:	121
Score:	385.00	Matches:	64
Percent Similarity:	65.49%	Conservative:	10
Best Local Similarity:	56.64%	Mismatches:	29
Query Match:	40.02%	Indels:	10
		Gaps:	1

US-09-914-324A-3 (1-508) x S66830 (1-121)

```

QY 19 ATGATGTGATATACCCGAGCGGACCAACAGCGGCGCGGC----- 60
DB 8 MetAspValAspGluAspGluSerGlnAsnIleAlaGlnSerSerAsnGlnSerAlaPro 27
QY 61 -----AAGAAGCGCTTGAAGTGAAGGATGGAATGCAGAGCGCTGGGCGC 108
DB 28 ValGlnThrLysLysArgPheGlnIleLysLysTyrThrAlaValAlaPheTyrPser 47
QY 109 TGGGATATGTGTTGATTAAGTGCATCTGCAGAACCAATTATGATCTTTGCATA 168
DB 48 TyrPspIleAlaValAlaAspAsnCysAlaIleCysArgAsnHisIleMetGluPyrCysIle 67
QY 169 GAATGTCAAGTCAACAGCGGCTCGGCTACTTCAGAGAGTGTACTGTGCGCATGGGAGTGC 228
DB 68 GluCysGlnProLysAlaMetGlnThrAspThrAspAsnGluCysValAlaAlaTyrGlyVal 87

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Db 2118 -----ThrValThrCysAspThrCysThrArgGluTyrHisTyrHisCysIle 2133
 QY 259 TCTGGCTGGCTCAAAACACAGACAGGTGTCTGCATTGGACACAGA 303
 |||||
 Db 2134 SerArgTTPLeuLysIleAsnSerValCysProGlnCysSerArg 2148
 |||||

RESULT 15

T06680

hypothetical protein T17F15.100 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 02-Sep-2000

C:Accession: T06680

R:Querier, F.; Choisme, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artigou

submitted to the Protein Sequence Database, April 1999

A:Reference number: 215793

A:Accession: T06680

A:Molecule type: DNA

A:Residues: 1-349 <QUE>

A:Cross-references: EMBL:AL049658; GSPDB:GN00061; ATSP:T17F15.100

A:Experimental source: cultivar Columbia; BAC clone T17F15

C:Genetics:

A:Gene: ATSP:T17F15.100

A:Map position: 3

A:Introns: 26/1; 81/2

C:Superfamily: RING finger homology

F:203-254/Domain: RING finger homology <RRN>

Alignment Scores:

Pred. No.:	0.00491	Length:	349
Score:	105.00	Matches:	23
Percent Similarity:	43.06%	Conservative:	8
Best local Similarity:	31.94%	Mismatches:	25
Query Match:	10.91%	Indels:	16
DB:	2	Gaps:	3

US-09-914-324a-3 (1-508) x T06680 (1-349)

QY 127 AACTGTGCATCTGCAGAAACACATTATGATCTTGCATAGATGCAAGCTAACAG 186
 |||||
 Db 206 AspCysAlaValCysLeuAsnGluPheSerAsp----- 216
 |||||
 QY 187 GCGTCCGCTACTTCAGAAAGTGTACTGTGCATGGGAGTCTGTAAACATGCTTTTCAC 246
 |||||
 Db 217 -----ThrAspLysLeuArgLeu---ProValCysSerHisAlaPheHis 231
 |||||
 QY 247 TTGCACTGCATCTCTCGCTGCCTCAAAACACAGAGTGTGCATTGGACAAACAGAGAG 306
 |||||
 Db 232 LeuHisCysIleAspThrTTPLeuLeuSerAsnSerThrCysProLeuCysArgArgSer 251
 |||||
 QY 307 TGGAAATTCCAAAG-----TATGGGCACTAGAAA 336
 |||||
 Db 252 LeuSerThrSerAsnValCysTyrAsnHisSerGlu 263
 |||||

Search completed: March 25, 2004, 09:24:24
 Job time : 19.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus.n2p model

Run on: March 25, 2004, 09:15:55 ; Search time 14 Seconds
(without alignments)
3778.806 Million cell updates/sec

Title: US-09-914-324A-3

Perfect score: 962
Sequence: 1 cccaataatgcgcagcagat.....aaagtcagtgatctctcg 508

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame_plus.n2p.model -DEV=xlp
-Q=/cgn2.1/USPTO_epool_p/US0914324/runatc_25032004_090846.8718/app_query.fasta.1.647
-DB=SwissProt 42 -OPMT=faolan -SUFFIX=esp -MINMATCH=0.1 -LOOPLC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=tbl -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0914324 @CCN 1.1.16 @runat 25032004 090846.8718 -NCPUS=6 -ICPU=3
-NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	616	64.0	108	1 RBX1_HUMAN	Q8A6Z8 homo sapien
2	604	62.8	108	1 RBX1_SALSA	Q8G964 salmo salar
3	534	55.5	108	1 RBXA_DROME	Q9WSE1 drosophila
4	514.5	53.5	118	1 RBXA_ARATH	Q940X7 arabidopsis
5	499	51.9	115	1 RBXB_ARATH	Q9AB00 arabidopsis
6	493	51.2	110	1 RBX1_CAEEL	Q23457 caenorhabdi
7	469	48.8	107	1 RBX1_SCHPO	Q13859 schizosacch
8	400.5	41.6	122	1 RBXA_DROME	Q9A1X0 drosophila
9	385	40.0	121	1 RBX1_YEAST	Q08473 saccharomyc
10	292	30.4	113	1 RBX2_HUMAN	Q9WZ16 homo sapien
11	290.5	30.2	113	1 RBX2_MOUSE	Q9WZ16 mus musculu
12	209	21.7	84	1 ANI1_MOUSE	Q9GXP9 mus musculu
13	208	21.6	84	1 ANI1_HUMAN	Q9GXP9 mus musculu
14	164.5	17.1	94	1 VIP3_SCHPO	Q9AB86 schizosacch
15	91	9.5	148	1 RN12_HUMAN	Q9Y225 mus musculu
16	90	9.4	600	1 RN12_MOUSE	Q9WZ16 mus musculu
17	88	9.1	161	1 YOUN_CAEEL	P30631 caenorhabdi
18	87	9.0	624	1 RN12_HUMAN	Q9HW22 homo sapien

19	86	8.9	326	1 PEXA_HUMAN	Q60683 homo sapien
20	86	8.9	419	1 PEXA_PICPA	Q92265 pictia pae
21	85.5	8.9	232	1 Z364_HUMAN	Q9Y415 homo sapien
22	85.5	9.3	474	1 KPY3_AGRVI	P70789 agrobacteri
23	84	8.7	796	1 PRH_ARATH	P48785 arabidopsis
24	83.5	8.7	115	1 YBR2_YEAST	P38239 saccharomyc
25	83	8.6	279	1 SLI3_HUMAN	Q14192 homo sapien
26	83	8.6	488	1 RNFG_MOUSE	Q8WC56 mus musculu
27	83	8.6	685	1 RNFG_HUMAN	Q9Y252 homo sapien
28	82.5	8.6	532	1 RNFG_MOUSE	P28990 equine herp
29	82.5	8.6	547	1 YDRD_SCHPO	Q13747 schizosacch
30	80.5	8.7	3703	1 ABFI_HUMAN	Q15911 homo sapien
31	80.5	8.7	3726	1 ABFI_MOUSE	Q61329 mus musculu
32	80	8.3	284	1 GOL1_DROME	Q06003 drosophila
33	80	8.3	583	1 YORF_SCHPO	Q9PFC1 schizosacch
34	79.5	8.3	305	1 Z364_MOUSE	Q9F0C1 mus musculu
35	79.5	8.3	437	1 PROE_MOUSE	P11680 mus musculu
36	79.5	8.6	482	1 KPY4_AGRVI	Q44473 agrobacteri
37	79.5	8.6	1221	1 TOP2_TRYBB	P12531 trypanosoma
38	79	8.2	381	1 RN13_CHICK	Q90972 gallus gall
39	79	8.2	381	1 RN13_HUMAN	Q43567 homo sapien
40	79	8.2	381	1 RN13_MOUSE	Q54965 mus musculu
41	79	8.2	410	1 ICPO_PRRVT	P29129 pseudorabie
42	79	8.2	1679	1 FUR2_DROME	P30432 drosophila
43	78.5	8.2	235	1 YQ57_CAEEL	Q09463 caenorhabdi
44	77.5	8.1	1493	1 M3K1_MOUSE	P53349 mus musculu
45	77	8.0	295	1 PEXA_PICAN	Q00940 pictia angu

ALIGNMENTS

RESULT 1
RBX1_HUMAN STANDARD: Q9Y254; PRT; 108 AA.
ID RBX1_HUMAN
AC Q8A6Z8; OS:US12; Q9WUK3; Q9Y254;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 43, Last annotation update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE RING-box protein 1 (Rbx1) (Regulator of cullins 1) (RING finger
protein 75) (zyp protein).
GN RBX1 OR ROCI OR RNF75.
OS Homo sapiens (Human), and
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606, 10090.
RN [1]
RP SEQUENCE FROM N.A., INTERACTION WITH CULLINS, AND MUTAGENESIS OF
RP CYS-53; CYS-56; CYS-75 AND HIS-77.
RC SPECIES=Human; TISSUE=Cervical carcinoma;
RX MEDLINE=99247022; PubMed=10230407;
RA Ohta T., Michel J.D., Schottelius A.J., Xiong Y.,
RT "ROCI, a homolog of Apcl1, represents a family of cullin partners with
an associated ubiquitin ligase activity.";
RL Mol. Cell 3:535-541(1999).
RN [2]
RP SEQUENCE FROM N.A., AND IDENTIFICATION IN CBC(VHL) COMPLEX.
RC SPECIES=Human, and Mouse;
RX MEDLINE=99234320; PubMed=10213691;
RA Kanura T., Koepf D.M., Conrad M.N., Skowrya D., Moreland R.J.,
RT Iliopoulos O., Lane W.S., Kaelin W.G. Jr., Ellledge S.J., Conway R.C.,
RA Harper J.W., Conway J.W.,
RT "Rbx1, a component of the VHL tumor suppressor complex and SCF
ubiquitin ligase.";
RL Science 284:657-661(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
RA Clamp M., Smink L.J., Alnough R., Almeida J.P., Babbage A.P.,
RA Bagley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,

RA Burdill W.D., Burton J., Carter C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis U., Dawson E.,
RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.W., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leverha M.A., Lloyd C., Lloyd D.M.,
RA Matyn I.D., Matherly S.A., McManis L.H., McMan O.T.,
RA McElroy J., McLaren S., McMurtry A.A., Milne S.A., Mortimore B.J.C.T.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vandin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyma S.,
RA Roe B.A., Chen F., Chu Y., Hu P., Hua A., Kenton S., Lai H., Do T.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malai E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaul S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Mink P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Oersky P., Rolfing T.,
RA Schreier P., Malke K., Latreille P., Layman D., Oersky P., Rolfing T.,
RA Kofler I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Salter S.,
RA Budarf M.L., McElmud H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Butler C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tiliakou Y., Wright H.,
RT "The DNA sequence of human chromosome 22.",
RL Nature 402:489-495(1999).
[4]
RN SEQUENCE FROM N.A.
RP SPECIES=Human, and Mouse; TISSUE=Brain, Mammary gland, and Placenta;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Nak S.I., Wang J., Heien F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Mulvaney S.J.,
RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullany S.W.,
RA Boeck S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalón D.K., Wuzny D.M., Sodergren E., Lu X., Gibbs R.A., Sanchez A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield J.S.N., Krzyzinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RN SEQUENCE FROM N.A.
RP SPECIES=Mouse; STRAIN=C57BL/6J; TISSUE=Embryo;
RC MEDLINE=22354683; PubMed=12468511;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Oseto N., Saito R., Suzuki H., Yamana K., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Brad D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Driscoll T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
RA Grammett S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kani A., Kawaji H., Kawasawa Y., Kedzierzki R.M., King P.A.,
RA Kongstad D.R., Kurochkin I.V., Lee Y., Lehman B., Lyons P.A.,
RA Maglott D.R., Maltz L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numa K., Okido T., Pavan W.J., Petrea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.V., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sulana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Watters C., Wang Y., Watanabe Y., Wells C.,
RA Wilting L.G., Wynshaw-Boris A., Yangisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Zimmet F., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Maki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analyses of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.",
RL Nature 420:563-573(2002).
[6]
RN SEQUENCE OF 14-108 FROM N.A.
RP SPECIES=Human, TISSUE=Brain;
RC MEDLINE=20106778; PubMed=10643962;
RA Perin U.-P., Seddigh N., Chattermeyer F., Goudou D., Belkadi L.,
RA Rieger F., Alliet P.M.,
RT "Genomic organization and expression of the ubiquitin-proteasome
complex-associated protein Rbx1/ROCI1/Hrt1.",
RL Cell. Mol. Biol. 45:1131-1137(1999).
[7]
RN SEQUENCE OF 92-105, INTERACTION WITH CUL1, AND
RP IDENTIFICATION IN A COMPLEX WITH CUL1, SKP1 AND SKP2.
RC SPECIES=Human, TISSUE=Cervical carcinoma;
RX MEDLINE=99247021; PubMed=10230406;
RA Tan P., Fuchs S.Y., Chen A., Wu K., Gomez C., Ronai Z., Pan Z.-O.,
RT "Recruitment of a ROCI1-CUL1 ubiquitin ligase by Skp1 and HOS to
catalyze the ubiquitination of I kappa B alpha.",
RL Mol. Cell 3:527-533(1999).
[8]
RN FUNCTION.
RP SPECIES=Human;
RX MEDLINE=20047893; PubMed=10579999;
RA Kamura T., Conrad M.N., Yan Q., Conaway R.C., Conaway J.W.,
RT "The Rbx1 subunit of SCF and VHL E3 ubiquitin ligase activates Rbx1
modification of cullins Cdc53 and Cul2.",
RL Genes Dev. 13:2928-2933(1999).
[9]
RN FUNCTION, AND SUBCELLULAR LOCATION.
RP SPECIES=Human;
RX MEDLINE=20481777; PubMed=11027288;
RA Furukawa M., Zhang Y., McCarville J., Ohta T., Xiong Y.,
RT "The CUL1 C-terminal sequence and ROCI are required for efficient
nuclear accumulation, NED8 modification, and ubiquitin ligase
activity of CUL1.",
RL Mol. Cell Biol. 20:8185-8197(2000).
[10]
RN IDENTIFICATION IN E3 UBIQUITIN LIGASE COMPLEX WITH MUF1, AND
RP IDENTIFICATION IN COMPLEXES WITH CUL5.
RC SPECIES=Human, and Mouse;
RX MEDLINE=21380117; PubMed=11384984;
RA Kamura T., Burian D., Yan Q., Schmidt S.L., Lane W.S., Querido E.,
RA Branton P.E., Shilatifard A., Conaway R.C., Conaway J.W.,
RT "Muf1, a novel elongin Bc-interacting leucine-rich repeat protein
that can assemble with Cul5 and Rbx1 to reconstitute a ubiquitin
ligase.",
RL J. Biol. Chem. 276:29748-29753(2001).
[11]
RN IDENTIFICATION IN E3 UBIQUITIN LIGASE COMPLEX WITH MED8.
RP SPECIES=Human;
RX MEDLINE=22155962; PubMed=12149480;

RA Brower C.S., Sato S., Tomomori-Sato C., Kamura T., Pause A.,
 RA Stearns R., Klausner R.D., Malik S., Lane W.S., Sorokina I.,
 RA Roeder R.G., Conway J.W., Conway R.C.,
 RT "Mammalian mediator subunit mMed8 is an Elongin Bc-interacting protein
 RT that can assemble with Cul2 and Rbx1 to reconstitute a ubiquitin
 RT ligase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:10353-10358(2002).
 RP IDENTIFICATION IN SCF-LIKE COMPLEX, AND INTERACTION WITH CUL7.
 RP SPECIES=Human;
 RX MEDLINE=22388271; PubMed=12481031;
 RA Dias D.C., Dolios G., Wang R., Pan Z.Q.,
 RT "CUL7: A DCC domain-containing cullin selectively binds Skp1, Fbx29 to
 RT form an SCF-like complex.";

Alignment Scores:
 Pred. No.: 2,23e-59 Length: 108
 Score: 616.00 Matches: 108
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 64.03% Indels: 0
 DB: 1 Gaps: 0

US-09-914-324A-3 (1-508) x RBX1_HUMAN (1-108)

QY 7 ATGGCGGCGCGCATGATGATGATACCCCGAGCGGCAACAGCGGCGGCGCAAGAG 66
 DB 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
 QY 67 CGCTTTAGAGTGAAGAAAGAGTGAATGCAGTACGCTCTGGGCTGGGATATTGGTTGAT 126
 DB 21 ArgPheGluValLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 40
 QY 127 AACTGTGCATTCGACGAGACCAATTCATTTTGCATTCATTCATTCATTCATTCAC 186
 DB 41 AsnCySalAlaIleCysArgAsnHisIleMetAspLeuCyIleGluCysAlaAsnGln 60
 QY 187 GGGTCGGCTACTTCGAGAGAGTGTACTGTGCGATGGGAGTGTGTACCATCTTTTAC 246
 DB 61 AlaSerAlaThrSerGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
 QY 247 TTCGACTGCATCTCTGCTGCTGCTCAAAACAGACGAGTGTGTCATTCGACACAGAG 306
 DB 81 PheHisCysIleSerArgTrpLeuLysTrpArgGlnValCysProLeuAspAsnArgLys 100
 QY 307 TGGGAATTCGCAAAAGATGGGAC 330
 DB 101 TrpGluPheGlnLysTrpLys 108
 RESULT 2
 RBX1_SALSA STANDARD; PRT; 108 AA.
 ID RBX1_SALSA
 AC 08064;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE RING-box protein 1 (Rbx1) (Hyperosmotic protein 21).
 OS RBX1 OR SHOR21.
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Proteobacteria; Salmoniformes; Salmonidae; Salmo.
 OC NCBI_TaxID=8030;
 ON 1;
 RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND INDUCTION.
 RP TISSUE=Gill;
 RX MEDLINE=22005592; PubMed=12010746;
 RA Pan F., Zarate J., Bradley T.M.,
 RT "A homolog of the E3 ubiquitin ligase Rbx1 is induced during
 RT hyperosmotic stress of salmon.";
 RT Am. J. Physiol. 282:R1643-R1653(2002).
 CC -!- FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) E3
 CC ubiquitin ligase complex, which mediates the ubiquitination and

CC subsequent proteasomal degradation of target proteins. Through the
 CC RING-type zinc finger, seems to recruit the E2 ubiquitination
 CC enzyme, like CDC34, to the complex and brings it into close
 CC proximity to the substrate (By similarity).
 CC -!- PATHWAY: Ubiquitin conjugation; third step.
 CC -!- SUBUNIT: Part of SCF complexes, which consist of SKP1, CUL1,
 CC RBX1 and a F-box protein (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed in heart and kidney.
 CC -!- INDUCTION: During hyperosmotic stress and thermal stress.
 CC -!- DOMAIN: The RING-type zinc finger domain is essential for
 CC ubiquitin ligase activity. It coordinates an additional third zinc
 CC atom.
 CC -!- SIMILARITY: Belongs to the RBX1 family.
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -----
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 CC -----
 CC DR EMBL; AY027936; AAK29182.1; ALT_INIT.
 CC DR InterPro; IPR001841; Znf_Ring.
 CC DR Pfam; PF00097; ZF-C3HC4_1.
 CC DR SMART; SM00184; RING; 1.
 CC DR PROSITE; PS50089; ZF_RING_2; 1.
 CC KM Ub1 conjugation pathway; Nuclear protein; Zinc; Zinc-finger;
 CC Metal-binding.
 CC FT ZN FING 53 98 RING-TYPE.
 CC FT METAL 42 42 ZINC 1 (BY SIMILARITY).
 CC FT METAL 45 45 ZINC 1 (BY SIMILARITY).
 CC FT METAL 53 53 ZINC 3 (BY SIMILARITY).
 CC FT METAL 56 56 ZINC 3 (BY SIMILARITY).
 CC FT METAL 68 68 ZINC 3 (BY SIMILARITY).
 CC FT METAL 75 75 ZINC 2 (BY SIMILARITY).
 CC FT METAL 77 77 ZINC 2 (BY SIMILARITY).
 CC FT METAL 80 80 ZINC 1 (BY SIMILARITY).
 CC FT METAL 82 82 ZINC 3 (BY SIMILARITY).
 CC FT METAL 83 83 ZINC 1 (BY SIMILARITY).
 CC FT METAL 94 94 ZINC 2 (BY SIMILARITY).
 CC FT METAL 97 97 ZINC 2 (BY SIMILARITY).
 CC SQ SEQUENCE 108 AA; 12318 MW; 44CB3A712CBDC7BB CRC64;
 Alignment Scores:
 Pred. No.: 4.61e-58 Length: 108
 Score: 604.00 Matches: 106
 Percent Similarity: 98.15% Conservative: 0
 Best Local Similarity: 98.15% Mismatches: 2
 Query Match: 62.79% Indels: 0
 DB: 1 Gaps: 0
 US-09-914-324A-3 (1-508) x RBX1_SALSA (1-108)
 QY 7 ATGGCGGCGCGCATGATGATGATACCCCGAGCGGCAACAGCGGCGGCGCAAGAG 66
 DB 1 MetAlaAlaAlaMetAspValAspThrProSerAlaThrAsnSerGlyAlaSerLysLys 20
 QY 67 CGCTTTAGAGTGAAGAAAGTGAATGCAGTACGCTCTGGGCTGGGATATTGGTTGAT 126
 DB 21 ArgPheGluValLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 40
 QY 127 AACTGTGCATTCGACGAGACCAATTCATTTTGCATTCATTCATTCATTCATTCAC 186
 DB 41 AsnCySalAlaIleCysArgAsnHisIleMetAspLeuCyIleGluCysAlaAsnGln 60
 QY 187 GGGTCGGCTACTTCGAGAGAGTGTACTGTGCGATGGGAGTGTGTACCATCTTTTAC 246
 DB 61 AlaSerAlaThrSerGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
 QY 247 TTCGACTGCATCTCTGCTGCTGCTCAAAACAGACGAGTGTGTCATTCGACACAGAG 306

Db 81 PhenixCysIleSerArgTyrLeuLysThrArgIleValCysProLeuAspAsnArgIle 100
 Cy 307 TGGGAATTCCTCAAGATATGGCGAC 330
 Db 101 TrrpLuphaginLysTyrGlyHis 108

RESULT 3
 ID RBXA DROME STANDARD; PRT; 108 AA.
 AC C9W5E1; C77429;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE RING-box protein 1A (Regulator of cullins 1a) (drbx1).
 GN ROCI1 OR CG16982 OR EG:115C2.11.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 CX NCBI_Taxid:7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceoliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richardson M., Ashburner S.N.,
 RA Sutton G.C., Wortman J.R., Yandell M.D., Zheng Q., Chen L.X.,
 RA Brandon R.C., Rogers J.H.C., Blake J.R.G., Chape M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Abmayri A., An H.-J., Andrews-Fiankhoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benise P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,
 RA Burtis K.C., Busan D.A., Butler J., Brockstein P., Broctier P.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodde K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hoston D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
 RA Idalmi M., Kalush F., Kapen G.H., Ke Z., Kemsion U.A., Ketchum K.A.,
 RA Kimali B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laske P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Moadary C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Murzy D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Pui V., Reese M.G.,
 RA Palaret K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Oregon-R;
 RX MEDLINE=20156011; PubMed=10731137;
 RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D., Cadieu E.,
 RA Barrett B.G., Ferraz C., Vidal S., Brun C., Demillies J., Brockstein P.,
 RA Dreeso S., Glouos F.C., Lelaure V., Mottier S., Galibert F., Borkova D.,
 RA Minna B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
 RA Papagianakis G., Spanos L., Cox S., Meduno E., de Pablos B.,
 RA Modolelli J., Peter A., Schoettler P., Werner M., Mourkioti F.,
 RA Beinert N., Dowe G., Schaefer U., Jaekle H., Bucheton A., S.,
 RA Callister D.M., Campbell L.A., Darlantisou A., Henderson N.S.,
 RA McMillan P.J., Sallies C., Tait E.A., Valenti P., Saunders R.D.C.,
 RA Glover D.M.;
 RT "From sequence to chromosome: the tip of the X chromosome of *D. melanogaster*.";
 RL Science 287:2220-2222(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Berkeley; TISSUE-Embryo;
 RX MEDLINE=2242606; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brockstein P., Yu C., Chape M.,
 RA George R.A., Guarini H., Krommiller B., Pauley J.M., Park S., Wan K.H.,
 RA Rubin G.M., Ceoliker S.E.;
 RT "A *Drosophila* full-length cDNA resource.";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 RN [4]
 RP FUNCTION, TISSUE SPECIFICITY, DEVELOPMENTAL STAGE, AND MUTAGENESIS OF
 ASN-59 AND CYS-68.
 RX MEDLINE=22057626; PubMed=12062088;
 RA Noureddine M.A., Donaldson T.D., Thacker S.A., Duronio R.J.,
 RT "Drosophila Roci1 encodes a RING-H2 protein with a unique function in
 processing the Hh signal transducer Ci by the SCF E3 ubiquitin
 ligase.";
 RL Dev. Cell 2:757-770(2002).
 RN [5]
 RP INTERACTION WITH LIN9 AND SLMB.
 RX MEDLINE=21391618; PubMed=11500045;
 RA Bocca S.N., Muzopappa M., Silberstein S., Wapner P.;
 RT "Occurrence of a putative SCF ubiquitin ligase complex in
Drosophila.";
 RL Biochem. Biophys. Res. Commun. 286:357-364(2001).
 RN [6]
 RP REVIEW ON E3 UBIQUITIN LIGASE COMPLEXES.
 RX MEDLINE=2273611; PubMed=12850443;
 RA Ou C.-Y., Pi H., Chien C.-T.;
 RT "Control of protein degradation by E3 ubiquitin ligases in *Drosophila*
 eye development.";
 RL Trends Genet. 19:382-389(2003).
 CC -1- FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) E3
 ubiquitin ligase complex, which mediates the ubiquitination and
 subsequent proteasomal degradation of target proteins. Through the
 RING-type zinc finger, seems to recruit the E2 ubiquitination
 enzyme to the complex and brings it into close proximity to the
 substrate. Required for the specific SCF-dependent proteolysis of
 Ct, but not that of Abm, suggesting that it also participates in
 the selection of substrates inside the SCF complex.
 CC -1- SUBUNIT: Part of a SCF complex consisting of SkpA (SKP1), Lin9
 (CUL1), Roc1A and F-box protein Slmb. Interacts directly with
 Lin9 and Slmb.
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Widely expressed. Expressed in embryonic,
 larval and adult tissues.
 CC -1- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
 CC -1- DOMAIN: The RING-type zinc finger domain is essential for
 ubiquitin ligase activity. It coordinates an additional third zinc
 atom (By similarity).
 CC -1- SIMILARITY: Belongs to the RING-box family.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous
 gene model prediction.
 CC -----
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 or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL; AF003418; AAF45536.1;
 CC EMBL; AL031581; CAA20888.1; ALT_SEQ.

DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE RING-box protein 1B (Regulator of cullins 1b).
DN ROCI1 OR ROCI2 OR CG1698B.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN RN
RN [1] _SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RP MEDLINE=22057626; PubMed=12065088;
RX Nouredidine M.A., Donaldson T.D., Thacker S.A., Duronio R.J.;
RT "Drosophila Roc1a encodes a RING-H2 protein with a unique function in
RT processing the Hn signal transducer Ci by the SCF E3 ubiquitin
RT ligase".
RL dev. Cell 2:757-770(2002).
RN RN
RN [2]
RP SEQUENCE FROM N.A.
RN RN
RN STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanalides P.G., Scherer S.E., Li P.W., Hoklins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.F.,
RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Peiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.W., Basu A., Baxendale J., Bayraktoglu D., Beasley E.M.,
RA Beeson K.Y., Benson P.V., Bernier B.P., Bhattacharya D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck T., Brockstein P., Brothier P.,
RA Butts K.C., Busam D.A., Butler H., Cadien B., Center A., Chandra I.,
RA Cherry J.M., Chesley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.U., Wei M.-H., Izbogam C.,
RA Jaitani M., Kalish F., Kapen G.H., Ke Z., Kemstun J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liak X., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskeken D.R., Paclob J.M.,
RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Sanders R.D.C., Scheller F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Slatk T.,
RA Spier E., Spreading A.C., Stapleton M., Strong R., Sun B.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weisencko G.M., Weissbach J.,
RA Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong G.W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.W., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*".
RL Science 287:2185-2195(2000).
RN RN
RN [3]
RP SEQUENCE FROM N.A.
RN RN
RN STRAIN=Berkeley; TISSUE=Testis;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brooksstein P., Yu C., Champe M.,
RA George R.A., Gaurin H., Krommiller B., Paclob J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A *Drosophila* full-length cDNA resource".
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC -!- FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) E3
CC ubiquitin ligase complex, which mediates the ubiquitination and
CC subsequent proteasomal degradation of target proteins. Through the
CC RING-type zinc finger, seems to recruit the E2 ubiquitination
CC enzyme to the complex and brings it into close proximity to the
CC substrate (by similarity).

CC -1- PATHWAY: Ubiquitin conjugation; third step.
 CC -1- SUBUNIT: Part of a SCF complex consisting of SkpA (SKP1),
 CC Ltn19 (CUL1), Roc1B and a F-box protein (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Highly expressed in early embryos, and in
 CC pupae. Widely expressed in adult males, while it is weakly
 CC expressed in adult females.
 CC -1- DOMAIN: The RING-type zinc finger domain is essential for
 CC ubiquitin ligase activity. It coordinates an additional third zinc
 CC atom (By similarity).
 CC -1- SIMILARITY: Belongs to the RING-box family.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-16 is the initiator.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC -----
 CC EMBL; AF218250; AAF32313.1; ALT_INIT.
 CC DR EMBL; AE003468; AAF47382.1; -.
 CC DR EMBL; AY070810; AAL48432.1; -.
 CC DR FLYBase; FBGN0040291; Roc1B.
 CC DR InterPro: IPR001841; Znf ring.
 CC DR Pfam; PF00097; ZF-C3HC4_1.
 CC DR SMART; SM00184; RING_1.
 CC DR PROSITE; PS50089; ZF_RING_2; 1.
 CC KW Ub1 conjugation pathway; Nuclear protein; Zinc; Zinc-finger;
 CC Metal-binding.
 CC
 CC FT ZN FING 57 112 RING-TYPE.
 CC METAL 68 68 ZINC 3 (BY SIMILARITY).
 CC FT METAL 71 71 ZINC 3 (BY SIMILARITY).
 CC FT METAL 82 82 ZINC 3 (BY SIMILARITY).
 CC FT METAL 96 96 ZINC 3 (BY SIMILARITY).
 CC FT METAL 57 57 ZINC 1 (BY SIMILARITY).
 CC FT METAL 60 60 ZINC 1 (BY SIMILARITY).
 CC FT METAL 89 89 ZINC 2 (BY SIMILARITY).
 CC FT METAL 91 91 ZINC 2 (BY SIMILARITY).
 CC FT METAL 94 94 ZINC 1 (BY SIMILARITY).
 CC FT METAL 97 97 ZINC 1 (BY SIMILARITY).
 CC FT METAL 108 108 ZINC 2 (BY SIMILARITY).
 CC FT METAL 111 111 ZINC 2 (BY SIMILARITY).
 CC FT METAL 111 111 ZINC 2 (BY SIMILARITY).
 CC SQ SEQUENCE 122 AA; 14225 MW; F22CE00438725410 CRC64;
 CC
 CC Alignment Scores:
 CC Pred. No.: 9,256-36 Length: 122
 CC Score: 400.50 Matches: 70
 CC Percent Similarity: 77.5% Conservative: 13
 CC Best Local Similarity: 65.4% Mismatches: 19
 CC Query Match: 41.63% Indels: 5
 CC DB: 1 Gaps: 2
 CC
 CC US-09-914-324A-3 (1-508) x RBXB_DROME (1-122) -----GGGGGGAAG 66
 CC QY 19 ATGATGTGGATACCCCGAGCGGCAACAGCGGC-----GGGGGGAAG 66
 CC DB 16 MetAaPheAsnAspGluGluProSerCysSerGlyGlyAlaValAlaAlaArgThrGlu 35
 CC QY 67 CGCTTTGAAGTGAAGAAAGTGAATGAGAGCCCTCTGGGCGCTGGGATATTGTGGTGTAT 126
 CC DB 36 ArgPheValValLysLysTyrValAlaHisAlaMetTTPGlyTyrPAspValAlaValAsp 55
 CC QY 127 AACGTGCGATCTGCGAGAACACATTTATGATCTTTTGCATRGATGTCACAGTAAACAG 186
 CC DB 56 AAcysAlaAlaLeCysArgAsnHisIleMetAsnLeuCySileGlyCysGlnAlaAsp--- 74
 CC QY 187 GGGTCGGCTACTGAGAGAGTGTACTGCGATGGGAGAGTGTGTAAACATGCTTTTAC. 246
 CC DB 75 ProAsnAlaAsnGlnAspGluCysThrValAlaTyrPglGluCysAsnHisAlaPheHis 94

QY 247 TTCACATGATCTCTCGCTGGCTCAAAACAGACAGGTGTGTCATTGACCAACAGAG 306
 DB 95 TyrHisCysIleAlaAlaGlyTyrPheLysThrArgLeuValCysProLeuAspAsnLysGlu 114
 QY 307 TGGGAATTCGAAAGATGGG 327
 DB 115 TrpValTyrGlnLysTyrGly 121
 RESULT 9
 REB1_YEAST STANDARD. PRT: 121 AA.
 ID REB1_YEAST
 AC Q08273;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE RING-box protein HRT1 (RING-box protein 1).
 GN HRT1 OR REB1 OR YOL133W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / FY1679;
 RX MEDLINE=97051593; PubMed=8896270;
 RA Alder M., Piedrafita L., Casas C., Casamayor A., Khalid H.,
 RA Balcells L., Arino J., Herrero E.;
 RT "Sequence analysis of a 12 801 bp fragment of the left arm of yeast
 RT chromosome XV containing a putative 6-phosphofructo-2-kinase gene, a
 RT gene for a possible glycopospholipid-anchored surface protein and
 RT six other open reading frames.";
 RL Yeast 12:1053-1058(1996).
 RN [2]
 RP SEQUENCE OF 8-31, FUNCTION, INTERACTION WITH CDC3; CDC4 AND
 RP CDC34, AND IDENTIFICATION IN SCF COMPLEX.
 RX MEDLINE=993115634; PubMed=10385629;
 RA Seol J.H., Feldman R.M.R., Zachariae W., Shevchenko A., Correll C.C.,
 RA Iyapina S., Chl Y., Galova M., Claypool J., Sandmeyer S., Nasmyth K.,
 RA Shevchenko A., Deshaies R.J.;
 RT "cdc3/cullin and the essential Hrt1 RING-H2 subunit of SCF define a
 RT ubiquitin ligase module that activates the E2 enzyme Cdc34.";
 RL Genes Dev. 13:1614-1626(1999).
 RN [3]
 RP IDENTIFICATION IN SCF COMPLEX, INTERACTION WITH CDC34 AND CDC4, AND
 RP MUTANT RBX1-1.
 RX MEDLINE=99234321; PubMed=10213692;
 RA Skoway D., Koepf D.M., Kamura T., Conrad M.N., Conaway R.C.,
 RA Conaway J.W., Elledge S.J., Harper J.W.;
 RT "Reconstitution of G1 cyclin ubiquitination with complexes containing
 RT SCFGrr1 and Rbx1.";
 RL Science 284:662-665(1999).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=20047893; PubMed=10579999;
 RA Kamura T., Conrad M.N., Yan Q., Conaway R.C., Conaway J.W.;
 RT "The Rbx1 subunit of SCF and Vhl E3 ubiquitin ligase activates Rub1
 RT modification of cullins Cdc53 and Cul2.";
 RL Genes Dev. 13:2928-2933(1999).
 RN [5]
 RP SUBCELLULAR LOCATION, AND MUTANT HRT1-C81Y.
 RX MEDLINE=20341308; PubMed=10880467;
 RA Blondel M., Galan J.-M., Peter M.;
 RT "Isolation and characterization of HRT1 using a genetic screen for
 RT mutants unable to degrade Glc2p in Saccharomyces cerevisiae.";
 RL Genetics 155:1033-1044(2000).
 CC -1- FUNCTION: Component of E3 ubiquitin ligase SCF complexes, which
 CC mediate the ubiquitination and subsequent proteasomal degradation
 CC of target proteins. Seems to recruit the E2 ubiquitination enzyme,
 CC like UBC3/CDC34, to the complex and brings it into close proximity
 CC to the substrate. Also stimulates UBC3/CDC34 autoubiquitination
 CC and promotes the neddylation of CDC34.
 CC -1- PATHWAY: Ubiquitin conjugation; third step.
 CC -1- SUBUNIT: Part of SCF E3 ubiquitin ligase complexes containing

R Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schler G.D.,
RA Altshuler S.F., Zeeberg B., Buettow K.H., Shenman C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish P.,
RA Diatchenko L., Marisusa K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E.,
RA Brownstein M.J., Soares W.B., Bonaldo M.P., Casavant P., Prange C.,
RA Roha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Beak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Huliyil S.W.,
RA Villalón D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzywinski M.T., Skalska U., Smalins D.E.,
RA Genereux A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
[7]
INTERACTION WITH CUL1, AND FUNCTION.
MEDLINE=20305864; PubMed=10851089;
RX Swaroop M., Wang Y., Miller P., Duan H., Jatkeo T., Madore S.J.,
RA Sun Y.;
RT "Yeast homolog of human SAG/RCC2/Rbx2/Hrt2 is essential for cell
growth, but not for germination: chip profiling implicates its role
in cell cycle regulation";
Oncogene 19:2855-2866(2000).
[8]
PHOSPHORYLATION BY CK2.
MEDLINE=22765595; PubMed=12746192;
RX Kim Y.-S., Lee J.-Y., Son M.-Y., Park W., Bae Y.-S.;
RT "Phosphorylation of threonine 10 on CKBP1/SAG/RCC2/Rbx2 by protein
kinase CKII promotes the degradation of IkappaBalpha and p27Kip1.";
J. Biol. Chem. 278:28462-28469(2003).
- I - FUNCTION: Probable component of the SCF (SKP1-CUL1-F-box protein)
E3 ubiquitin ligase complex which mediates the ubiquitination and
subsequent proteasomal degradation of target proteins involved in
cell cycle progression, signal transduction and transcription.
Through the RING-type zinc finger, seems to recruit the E2
ubiquitination enzyme to the complex and brings it into close
proximity to the substrate. May play a role in protecting cells
from apoptosis induced by redox agents.
- I - PATHWAY: Ubiquitin conjugation; third step.
- I - SUBUNIT: Probable part of SCF complexes, which consist of SKP1,
CUL1, NEMO/RBX2 and a F-box protein. Interacts with CUL1, CUL2,
CUL3, CUL4A, CUL4B and CUL5. Interacts with CSNK2B, the
interaction is not affected by phosphorylation by CK2.
- I - SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
- I - ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1;
IsoId=GQUBFc-1; Sequence=Displayed;
Name=2; Synonyms=SAC-V;
IsoId=GQUBFc-2; Sequence=VSP_008449;
Note=Inactive!
- I - TISSUE SPECIFICITY: Expressed in heart, liver, skeletal muscle and
pancreas. At very low levels expressed in brain, placenta and
lung.
- I - INDUCTION: By 1,10-phenanthroline.
- I - DOMAIN: The RING-type zinc finger domain is essential for
ubiquitin ligase activity. It coordinates an additional third zinc
atom.
- I - PTM: Phosphorylation by CK2 is required for efficient degradation
of NFkBIA and CDKN1B.
- I - SIMILARITY: Belongs to the RING-box family.
- I - SIMILARITY: Contains 1 RING-type zinc finger.

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CC      entities requires a license agreement (see http://www.lsb-slb.ch/announce/
CC      or send an email to license@lsb-slb.ch).
CC
DR      EMBL; AF164679; AAD55964.1; -
DR      EMBL; AF142060; AAD30147.1; -
DR      EMBL; AF092878; AAD25962.1; -
DR      EMBL; AF312226; AAQ37450.1; -
DR      EMBL; BT007348; AAA36012.1; -
DR      EMBL; BC005966; AAH05966.1; -
DR      EMBL; BC008627; AAH08627.1; -
DR      MIM; 603863; -
DR      InterPro; IPR001841; Znf_fing.
DR      Pfam; PF00097; zf-C3HC4; 1.
DR      SMART; SM00184; RING; 1.
DR      PROSITE; PS50089; ZF_RING_2; 1.
KW      Ubl conjugation pathway; Zinc; zinc-finger; Metal-binding;
KW      Phosphorylation; Alternative splicing.
FT     ZN FING        61          103
FT     METAL          50          50
FT     METAL          53          53
FT     METAL          61          61
FT     METAL          64          64
FT     METAL          73          73
FT     METAL          80          80
FT     METAL          82          82
FT     METAL          85          85
FT     METAL          87          87
FT     METAL          88          88
FT     METAL          98          99
FT     METAL          102         102
FT     MOD_RES        10          10
FT     VARSP_LIC      60          113
SQ     CONFLICT       23          23
FT     SEQUENCE       113 AA; 12663 MW; CE1B6CAC940C8257 CRC64;
                                K -> T (IN REF. 2).
                                /FTID=VSP_008449.

Alignment Scores:
Pred. No.:           7.05e-24
Score:              292.00
Percent Similarity: 64.95%
Best Local Similarity: 50.52%
Query Match:        30.35%
DB:                  1

US-09-914-324A-3 (1-508) x RBX2_HUMAN (1-113)
QY      37 AGCGGACCAACAAGCGCGCGGACAGAAGCGCTTGAAGTAAAAAGTGAAATGCAGTA 96
                |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Dd      20 SerGIserIySerIy---giyaeplysmetPheSerleuIySerIyStrpaMaIval 38
QY      97 GCCCTGTGGGCCCTGGGATAATTGGTTGATTAACGTGGCATTCGACAGAACACATTATG 156
                |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Dd      39 AlameTriserIyStrpaValglucysabepmrcysalallecysargValgInvalmec 58
QY      157 GATCTTGGATGAAGATGTCAAGCTTAACAAGCGCTCGCTACTTCAAGAAGTGTACTGTC 216
                |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Dd      59 AsphAlCybleuArgcysglnalaIglaun-----LygslngInubspCysValval 75
QY      217 GCATGGGAGAGCTGTATAACATGCTTTTCACTTCCATGCATCTCTCGCTGGCTCAAAAACA 276
                |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Dd      76 ValITrgIyGlucysasnhIsseIPheHLSaeRCysCysWeseterleutrpValylsgln 95
QY      277 CGACAGAGTGTGCATTGGACACAAGAGTGGAAATTCCAAAGATATGGG 327
                |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Dd      96 AsnaahArgCysproleucysglnInaspIrpValValgInArgIllegly 112

RESULT 11
RBX2_MOUSE
ID      _RBX2_MOUSE STANDARD; PRT; 113 AA.
QC      QSWTZ1;
```

DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE RING-box protein 2 (Rbx2) (RING finger protein 7) (Sensitive to
 apoptosis gene product).
 GN RNF7 OR Rbx2 OR SAG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA, TISSUE=Lung;
 RX MEDLINE=9182502; PubMed=10082581;
 RA Duan H., Wang Y., Aviram M., Swaroop M., Loo J.A., Bian J., Tian Y.,
 RA Mueller T., Bigatler C.L., Sun Y.,
 RT "SAG, a novel zinc RING finger protein that protects cells from
 apoptosis induced by redox agents,"
 RL Mol. Cell. Biol. 19:3145-3155 (1999).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J, TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka S.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa I., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleishmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai J., Okido T., Furuno M., Aono H., Baldarelli P., Bash G.,
 RA Blake J., Boftelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Holman M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombearts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohseki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection,"
 RL Nature 409:685-690 (2001).
 [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Scheetz T.E.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Bosak S.S., McLean P.J., McKernan K.J., Malek J.A., Guarniere P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulvik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonifard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerf A., Schein U.E., Jones S.U.W., Natta W.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences,"
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: Probable component of the SCF (SKP1-CUL1-F-box protein)
 CC E3 ubiquitin ligase complex which mediates the ubiquitination and
 CC subsequent proteasomal degradation of target proteins involved in
 CC cell cycle progression, signal transduction and transcription.
 CC Through the RING-type zinc finger, seems to recruit the E2
 CC ubiquitination enzyme to the complex and brings it into close

CC proximity to the substrate. May play a role in protecting cells
 CC from apoptosis induced by redox agents.
 CC -1- PATHWAY: Ubiquitin conjugation; third step.
 CC -1- SUBUNIT: Probable part of SCF complexes, which consist of SKP1,
 CC CUL1, RNF7/Rbx2 and a F-box protein. Interacts with CUL1, CUL2,
 CC CUL3, CUL4A, CUL4B, CUL5 and CSN2B (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
 CC -1- DOMAIN: The RING-type zinc finger domain is essential for
 CC ubiquitin ligase activity. It coordinates an additional third zinc
 CC atom.
 CC -1- SIMILARITY: Belongs to the RING-box family.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).

CC EMBL; AF092877; AA025961.1; -
 CC EMBL; AK003248; BA02566.1; -
 CC EMBL; BC01127; AA01127.1; -
 CC MGD; MG1:1337096; Rnf7.
 CC GO; GO:0005737; C:cytoplasm; IDA.
 CC GO; GO:0005634; C:nucleus; IDA.
 CC GO; GO:0006916; P:anti-apoptosis; IDA.
 CC GO; GO:0008637; P:apoptotic mitochondrial changes; IDA.
 CC GO; GO:0006919; P:caspase activation; IDA.
 CC GO; GO:0008631; P:induction of apoptosis by oxidative stress; IDA.
 CC InterPro; IPR001841; Znf_C1HC4.1.
 CC Pfam; PF00097; zf-C3HC4.1.
 CC SMART; SM00184; RING.1.
 CC PROSITE; PS00089; ZF_RING_2; 1.
 CC UBL conjugation pathway; Zinc; Zinc-finger; Metal-binding.
 CC ZN_FING
 CC FT METAL 50 50 RING 1 (BY SIMILARITY)
 CC FT METAL 53 53 ZINC 1 (BY SIMILARITY)
 CC FT METAL 61 61 ZINC 3 (BY SIMILARITY)
 CC FT METAL 64 64 ZINC 3 (BY SIMILARITY)
 CC FT METAL 73 73 ZINC 3 (BY SIMILARITY)
 CC FT METAL 80 80 ZINC 2 (BY SIMILARITY)
 CC FT METAL 82 82 ZINC 1 (BY SIMILARITY)
 CC FT METAL 85 85 ZINC 1 (BY SIMILARITY)
 CC FT METAL 87 87 ZINC 3 (BY SIMILARITY)
 CC FT METAL 88 88 ZINC 1 (BY SIMILARITY)
 CC FT METAL 99 99 ZINC 2 (BY SIMILARITY)
 CC FT METAL 102 102 ZINC 2 (BY SIMILARITY)
 CC SEQUENCE 113 AA; 12707 MW; D6FA02EB6038FDD2 CRC64;

Alignment Scores:
 Pred. No.: 1,03e-23 Length: 113
 Score: 290.50 Matches: 52
 Percent Similarity: 58.62% Conservative: 16
 Best Local Similarity: 44.83% Mismatches: 35
 Query Match: 30.20% Indels: 13
 DB: 1 Gaps: 3

US-09-914-324A-3 (1-508) X RBX2_MOUSE (1-113)
 QY 7 ATGGCGGACGATGATGATGATACCCG-----AGC 39
 DB 1 MetAlaAspValGluAlaPglYgluGluProCyValLeuSerSerHisSerGlySerAla 20
 QY 40 GGCAACCAACGCGCGCGCGGACAGAACCGCTTTCAGATGAAGAAAGTGAATGAGTCC 99
 DB 21 GlySerYssSerGly---GlyAspLysMetPheSerLeuYsYsItpAsnAlaValAla 39
 QY 100 CTCGCGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 159
 DB 40 MetItpSerItpAspValGluGluCyAspThrCyAlaIleCyAspValGluValMetAsp 59

CC 160 CTTGCAATAGATGCAAGCTACAGGCGTCCGCTACTTACAGAGTACTGTGCA 219
 CC 60 AlACysleuArgCysGlnAlaGluAsn-----LysGlnGlnAspCysValValVal 76
 CC 220 TGGGAGTGTGTGTAACCACTGCTTTTCACTTCCACTGATCTTCTGCTGCTCAAAACAGA 279
 CC 77 TrrglYglucysAsnHisserPheHisAsnCysCysMetserNeutrpValLysGlnAsn 96
 CC 280 CAGGTGTGCTGCTGCAACAGAGTGGAGTTCGAAATGCAAGATGGG 327
 CC 97 AsnArgCysProleuCysGlnGlnAspTrpValValAlaTrpArgLgely 112
 CC 12
 CC AN11_MOUSE STANDARD; PRT; 84 AA.
 CC 16-OCT-2001 (Rel. 40, Created)
 CC 16-OCT-2001 (Rel. 40, Last sequence update)
 CC 10-OCT-2003 (Rel. 42, Last annotation update)
 CC Anaphase promoting complex subunit 11 (APC11) (Cyclosome subunit 11).
 CC ANAPC11.
 CC Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina, and Embryo;
 CC MEDLINE=22354683; PubMed=12466851;
 CC OKazaki Y., Furuno M., Kasukawa T., Adachi Y., Bono H., Kondo S.,
 CC Nishida I., Osato N., Saito R., Suzuki H., Yamanka I., Kiyosawa H.,
 CC Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gotohori T.,
 CC Baldarelli R., Hill D.P., Bull C., Hume D.A., Quakehush J.,
 CC Schmitt L.M., Kanapin A., Matunda H., Batilov S., Beisel K.W.,
 CC Blake J.A., Brad D., Bruscia V., Chochia C., Corbani L.E., Cousins S.,
 CC Dalla B., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 CC Gassterland T., Gariboldi M., Giasi C., Godzik A., Gough J.,
 CC Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 CC Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 CC Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 CC Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 CC Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
 CC Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 CC Ravasi T., Reed J.C., Reed J., Reid J., Ring B.Z., Ringwald M.,
 CC Sadelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 CC Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 CC Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 CC Wilting L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 CC Yuan Z., Zavoitan M., Zhu Y., Zimmer A., Carrinzi P., Hayatsu N.,
 CC Hirazane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 CC Shiraki T., Miki K., Kawai J., Alzawa K., Akakawa T., Fukuda S.,
 CC Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 CC Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 CC Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 CC Birney E., Hayashizaki Y.,
 CC "Analysis of the mouse transcriptome based on functional annotation of
 CC 60,770 full-length cDNAs";
 CC Nature 420:563-573 (2002).
 CC -!- FUNCTION: Component of the anaphase promoting complex/cyclosome
 CC (APC/C), a cell cycle-regulated ubiquitin ligase that controls
 CC progression through mitosis and the G1 phase of the cell cycle.
 CC May recruit the E2 ubiquitin-conjugating enzyme to the complex (By
 CC similarity).
 CC -!- PATHWAY: Ubiquitin conjugation; third step.
 CC -!- SUBUNIT: The APC/C is composed of at least 11 subunits. Interacts
 CC with the cullin domain of ANAPC2. Interacts with UBED22 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
 CC -!- DOMAIN: The RING-type zinc finger domain coordinates an additional
 CC third zinc atom (By similarity).
 CC -!- PTM: Auto-ubiquitinated (By similarity).
 CC -!- SIMILARITY: Belongs to the RING-box family.
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

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 CC or send an email to license@ebi.ac.uk).

CC EMBL: AK003244; BAB22663.1; -
 CC EMBL: AK003612; BAB22890.1; -
 CC EMBL: AK003686; BAB22937.1; -
 CC EMBL: AK045408; BAB22348.1; -
 CC MGD: MGI:1913406; Anapc11.
 CC InterPro: IPR001841; Znf_ring.
 CC SMART: SM00184; RING, 1.
 CC PROSITE: PS50089; ZF_RING_2; 1.
 CC Ubl conjugation pathway; Cell cycle; Cell division; Mitosis; Zinc;
 CC Zinc-finger; Metal-binding; Nuclear protein; Ubl conjugation.
 CC ZN_FING 34 77
 CC FT METAL 23 23 ZINC 1 (BY SIMILARITY).
 CC FT METAL 26 26 ZINC 1 (BY SIMILARITY).
 CC FT METAL 34 34 ZINC 3 (BY SIMILARITY).
 CC FT METAL 37 37 ZINC 3 (BY SIMILARITY).
 CC FT METAL 44 44 ZINC 3 (BY SIMILARITY).
 CC FT METAL 51 51 ZINC 2 (BY SIMILARITY).
 CC FT METAL 53 53 ZINC 2 (BY SIMILARITY).
 CC FT METAL 56 56 ZINC 1 (BY SIMILARITY).
 CC FT METAL 58 58 ZINC 3 (BY SIMILARITY).
 CC FT METAL 59 59 ZINC 1 (BY SIMILARITY).
 CC FT METAL 73 73 ZINC 2 (BY SIMILARITY).
 CC FT METAL 76 76 ZINC 2 (BY SIMILARITY).
 CC SQ SEQUENCE 84 AA; 9818 MW; EACBD5A194FC11AE CRC64;

Alignment Scores:
 Pred. No.: 8,336-15
 Score: 209.00
 Percent Similarity: 56.82%
 Best Local Similarity: 37.50%
 Query Match: 21.73%
 DB: 1 Gaps: 2

US-09-914-324A-3 (1-508) x AN11_MOUSE (1-84)

CC 67 CGCTTGAAGTGAAGAAAGTGAATGAGTACGAGCCCTGCGCTGCGATATGCTTGAT 126
 CC 2 LysValValIleLysGlySerTrpPheGlyValAlaThrTrpLeuTrpValAlaAsnAspGlu 21
 CC 127 AACTGCGCATCTGCGAGGAAACCACTTATGATCTTTGATGATGATGCAAGCTAACGAG 186
 CC 22 AsnCysGlyIleCysArgMetAlaPheAsnGlyCysCysProAspCysValys----- 38
 CC 187 GCGTCGCTACTTCCAGAAAGTACTGTGCGATGGGAGGTGTGTAACCACTTTTAC 246
 CC 39 -----ValProGlyAspAspCysProLeuValTrpGlyGlnCysSerHisCysPheHis 56
 CC 247 TTTCATGTCATCTGCTGCGCTGCTCAAAACAGACAGCGTG-----TGTCAATGAGC 297
 CC 57 MetHisCysIleLeuArgTrpLeuAsnAlaGlnValGlnGlnHisCysProMetCys 76
 CC 298 AACAGAGTGGGATTCGAAAG 321
 CC 77 ArgGlnGluTrpLysPheLysGlu 84

RESULT 13
 CC AN11_HUMAN STANDARD; PRT; 84 AA.
 CC 16-OCT-2001 (Rel. 40, Created)
 CC 16-OCT-2001 (Rel. 40, Last sequence update)
 CC 15-MAR-2004 (Rel. 43, Last annotation update)
 CC Anaphase promoting complex subunit 11 (APC11) (Cyclosome subunit 11)
 CC (Hepatocellular carcinoma associated RING finger protein) (HSPC214).

ID	RNA24	HUMAN	STANDARD	PR1	148 AA.
AC	09y225	OSUWH1			
DT	28-FEB-2003	(Rel. 41, Created)			
DT	28-FEB-2003	(Rel. 41, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	RING finger protein 24.				
GN	RNF24.				
OC	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21638749; PubMed=11780052;				
RA	Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,				
RA	Jones M., Stuvrives G., Almeida J.P., Babbage A.K., Baggaley C.L.,				
RA	Bailey J., Beirrow K.F., Bates K.N., Beard L.M., Beare D.M.,				
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.U.,				
RA	Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,				
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,				
RA	Cheng S., Cobley V.E., Collier R.E., Connor R.E., Corry N.R.,				
RA	Collison A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,				
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,				
RA	Grieffman D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,				
RA	Hammond S., Harley J.L., Heath F.D., Ho S., Holden J.L., Hovden P.J.,				
RA	Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,				
RA	Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,				
RA	Levanachach M.H., Levensha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,				
RA	Marsh V.L., Martin S.L., McConachie L.J., McIay K., McMurtry A.A.,				
RA	Malne S.A., Mistry D., Moore M.J.F., Mullikin J.C., McKernson T.,				
RA	Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,				
RA	Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,				
RA	Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,				
RA	Skuse C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,				
RA	Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,				
RA	Tracey A.C., Tromans A.C., Vardim M., Wall M., Wallis J.M.,				
RA	Whitehead S.L., Whitlaker P., Willey D.L., Williams L., Williams S.A.,				
RA	Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,				
RA	Rogers J.				
RT	"The DNA sequence and comparative analysis of human chromosome 20.";				
RL	Nature 414:865-871(2001).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Blood, and Kidney;				
RX	MEDLINE=22386257; PubMed=12477932;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Steinem C.M., Schuler G.D.,				
RA	Altshul S.F., Zeeberg B., Batetow K.H., Schaefer C.F., Bat N.K.,				
RA	Hopkins R.F., Jordan K.H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Stapchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldi M.F., Cassavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Udell T.B., Toibiyuki S., Carninci P., Pandey C.,				
RA	Rahm S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,				
RA	Boesk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				

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-----
DR      EMBL; AL096778; CAB46627.1; -
DR      EMBL; AL031670; CAB43182.1; -
DR      EMBL; BC000213; AAH00213.1; -
DR      EMBL; BC039584; AAH39584.1; -
DR      EMBL; AC079313; CAB45279.1; -
DR      HSSP; P28990; ICRC.
DR      Genew; HGNC:13779; RNF24.
DR      InterPro; IPR001841; ZnfRING.
DR      Pfam; PF00097; ZF-C3HC4; 1.
DR      SMART; SM00184; RING; 1.
DR      PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR      PROSITE; PS50089; ZF_RING_2; 1.
DR      Kyr   Zinc-finger.
FT      ZN_RING.      78      119
FT      CONFLICT      45      45      Y--S (IN REF. 3).
SQ      SEQUENCE      148 AA; 17209 MW; 66C240C3A591EAS CRC64;
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Alignment Scores:
Score: Pred. No.:
Score: 0.0772 Length: 148
Percent Similarity: 75.00% Matches: 14
Best Local Similarity: 58.33% Conservatve: 14
Query Match: 9.46% Mismatches: 6
DB: 1 Indels: 0 Gaps: 0
US-09-914-324A-3 (1-508) x RN24_HUMAN (1-148)
OY      229 TGTAAACCAAGCTTTTTCACATTCGATGCTGAGTCAAAAACAGACAGATGTGT 288
Db      96 CysLysNH:AdAlaPheNH:ArgLysCysLeuNH:ArgLysGluValAlaArgLysValCys 115
OY      289 CCATTGGACAC 300
Db      116 ProteoCysasn 119

```

Search completed: March 25, 2004, 09:21:57
Job time : 15 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 25, 2004, 09:17:20 / Search time 43 Seconds
(without alignments)
7455.035 Million cell updates/sec

Title: US-09-914-324a-3

Percent score: 962
Sequence: 1 cccaaaatggcggcagcgat.....aaagtcacgttcgattctcg 508

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Rgapop 6.0, Rgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2034082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODE=frame+np.model -DEV=xip
-O=/cgm2/1/USP70.spool.p/US09914324/runat.25032004.090847.8730/app.query.fasta.1.647
-DB=SPRMBL.25 -CPMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOCPCT=0 -LOCPXT=0
-UNITS=bites -START=1 -END=1 -MATRIX=blonum40.cai -LIST=45
-DOCLLEN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USR=US09914324 @CGN 1.1.86 @runat.25032004.090847.8730 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEOUTERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPRMBL.25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvtnus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	523.5	54.4	114	10 Q8S350

Result ID	Score	Query Match Length	ID	Description
2	523	54.4	110	10 Q7Y042
3	416	39.3	122	11 Q9D105
4	378	33.7	107	10 Q7Z657
5	314.5	32.7	97	10 Q9FTN1
6	308	32.0	92	5 Q8SM06
7	284.5	29.6	113	5 Q9V607
8	266	27.7	112	5 P91404
9	210	21.8	84	10 Q940X6
10	198	20.6	84	10 Q8J306
11	197	20.5	85	5 Q9V155
12	151	15.7	89	5 Q8IC08
13	146.5	15.2	135	5 Q20052
14	141	14.7	57	10 Q9M910
15	136	14.1	165	3 Q12157
16	132.5	13.8	99	10 Q9AV25
17	129.5	13.5	94	3 Q862L9
18	120.5	13.1	129	3 Q08272
19	116.5	12.1	2160	5 Q17709
20	112.5	11.7	911	3 Q96UD5
21	106.5	11.1	189	10 Q94U02
22	106	11.0	445	12 Q8QX10
23	105	10.9	349	10 Q9SU06
24	104	10.8	693	5 Q8U1U7
25	102.5	10.7	249	10 Q9C455
26	102.5	10.6	383	10 Q7X1Y9
27	102	10.6	151	10 Q9F195
28	102	10.6	210	10 Q9SD55
29	100	10.4	147	10 Q91JY5
30	100	10.4	650	10 Q84W43
31	100	10.4	676	10 Q9M1S2
32	99.5	10.3	207	5 Q7Y1Y5
33	99	10.3	524	10 Q815X8
34	99	10.3	494	10 Q9M1L1
35	98.5	10.2	571	3 Q94400
36	98	10.2	147	10 Q84WU1
37	98	10.2	158	10 Q9SPM0
38	97.5	10.1	272	10 Q9FHA1
39	97.5	10.1	295	10 Q8H740
40	97.5	10.1	327	10 Q9C711
41	97.5	10.1	445	5 Q81DY8
42	97	10.1	159	10 Q9LZV8
43	96.5	10.0	200	10 Q9ZT49
44	96.5	10.0	332	10 Q9L0M2
45	95.5	9.9	233	10 Q9FS27

ALIGNMENTS

RESULT 1
Q8S350 PRELIMINARY; PRT; 114 AA.
AC Q8S350;
DT 01-JUN-2002 (TREMBL) 21, Created
DT 01-JUN-2002 (TREMBL) 21, Last sequence update
DT 01-JUN-2003 (TREMBL) 24, Last annotation update
DE Putative ring box-1 protein.
GN 49P11.12.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
CX NCBI_TaxID=39947;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Park Y.-J., Roostoks N., Ramakrishna W., Samiuel P., Shiloff B.,
Ma J., Jiang Z., Kleinhofs A., Bennetzen J.;
RT "Sequence characterization of orthologous regions in the barley and rice genomes."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF480496; AAL87158.1; -;
DR Gramene; Q8S350; -;
DR InterPro; IPR001841; ZnF_ring.

DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00164; RING; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 SQ SEQUENCE 114 AA; 12754 MW; 568C63E0D733DD5C CRC64;

Alignment Scores:
 Pred. No.: 4.2e-52 Length: 114
 Score: 523.50 Matches: 92
 Percent Similarity: 89.91% Conservative: 6
 Best Local Similarity: 84.40% Mismatches: 10
 Query Match: 54.42% Indels: 1
 DB: 10 Gaps: 1

US-09-914-324A-3 (1-508) x Q8S3S0 (1-114)

QY 7 ATGGCGCGGATGATGTGATACCCGAGCGCAACAGCGCGGCGGCAAG--- 63
 DB ValAlaValAlaValProPseSerLeAlaGlyAlaSerSerSerLeAlaValVal 25
 QY 64 AACCGCTTTGAAGTGAAGAAAGTGAATGACAGCCCTCGGCGCTGGGATATTGTGTT 123
 DB LysArgHegHegLileuLysLysLysLysLysLysLysLysLysLysLysLysLys 45
 QY 124 GATTAAGTGTGATCTCTGAGAGAACACATATGATCTTTGATAGATGCAAGCTAAC 183
 DB AspAsnGysAlaIleCysArgAsnHisIleMetAspLeuGlyGlnAlaAsn 65
 QY 184 CAGCGCTCCGCTACTTGAAGAGAGTGTACTGTGCAATGGGAGTGTGTAACATGCTTT 243
 DB GluAlaSerAlaThrSerGluGluGluGluGluGluGluGluGluGluGluGluGlu 85
 QY 244 CACTTCACATGATCTCTGCTGCTGCTTAAACACAGAGGTGTGTCATTTGACACACA 303
 DB HisPheHisCysIleSerArgTrpLeuLysThrArgLysValCysProLeuAspAsnSer 105
 QY 304 GAGTGGAGATCCCAAGATGAGGAC 330
 DB GluTrpGluPheGlnLysTrpGlyHis 114

RESULT 2

QY042 PRELIMINARY; PRT; 110 AA.
 ID QY042;
 AC QY042;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Ring box protein.
 OS Populus tomentosa.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eucosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
 CX NCBI_TaxID=118781;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fan J.H.;
 RT "Ring-box protein (PcRbx1) of Populus tomentosa."
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY302066; AAF57304.1; -
 SQ SEQUENCE 110 AA; 12591 MW; 0172CGCAE3FA2772 CRC64;

Alignment Scores:

Pred. No.: 4.78e-52 Length: 110
 Score: 523.00 Matches: 93
 Percent Similarity: 88.18% Conservative: 4
 Best Local Similarity: 84.55% Mismatches: 7
 Query Match: 54.37% Indels: 6
 DB: 10 Gaps: 2

US-09-914-324A-3 (1-508) x QY042 (1-110)

QY 19 ATGATGTGAT-----ACCCGAGCGG-----ACCAACAGCGGCGGCGG 60
 DB 1 MetAspTrnAspValThrMetValProAlaGlyGluAlaSerSerSerSerArgLys 20

QY 61 AAGAGCGCTTTGAAGTGAAGAAAGTGAATGACAGCCCTCGGCGCTGGGATATTGTG 120
 DB 21 ProLysArgHegHegLileuLysLysLysLysLysLysLysLysLysLysLysLys 40
 QY 121 GTTATTAAGTGTGATCTCTGAGAGAACACATATGATCTTTGATAGATGCAAGCT 180
 DB ValAspAsnGysAlaIleCysArgAsnHisIleMetAspLeuGlyGlnAla 60
 QY 181 AACCGAGTCCGCTACTTGAAGAGAGTGTACTGTGCGCATGGGAGTGTGTAACATGCT 240
 DB AsnGlnAlaSerAlaThrSerGluGluGluGluGluGluGluGluGluGluGluGlu 80
 QY 241 TTTCACTTCACATGATCTCTGCTGCTGCTTAAACACAGAGGTGTGTCATTTGACAC 300
 DB PheHisPheHisCysIleSerArgTrpLeuLysThrArgLysValCysProLeuAspAsn 100
 QY 301 AGAGTGGGAGATCCCAAGATGAGGAC 330
 DB 101 SerGluTrpGluPheGlnLysTrpGlyHis 110

RESULT 3

QY0105 PRELIMINARY; PRT; 122 AA.
 ID QY0105;
 AC QY0105;
 DT 01-UN-2001 (TREMBLrel. 17, Created)
 DT 01-UN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE 1500002P1SR1k protein.
 GN BEX1 OR 1500002P1SR1K.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J, Shiragawa A, Shibata K, Yoshino M, Itoh M, Ishii Y,
 RA Arakawa T, Hara A, Fukunishi Y, Kono H, Adachi J, Fukuda S,
 RA Aizawa K, Izawa M, Nishi K, Kiyosawa H, Kondo S, Yamazaki I,
 RA Satoh T, Okazaki Y, Gojohori T, Bono H, Kanekawa T, Saito R,
 RA Kadota K, Matsuda H, Ashburner M, Batalov S, Casavant T,
 RA Fleischiemann W, Gaasterland T, Gissi C, King B, Kochwa H,
 RA Kuehl P, Lewis S, Matsumoto Y, Nakado I, Pesole G, Quackenbush J,
 RA Schriml L.M., Staahl F, Suzuki R, Tomita M, Wagner L, Washio T,
 RA Sakai K, Okido T, Furuno M, Aono H, Baldarelli R, Barch G,
 RA Blake J, Boffelli D, Bojunga N, Carninci P, de Bonaldo M.F.,
 RA Brownstein M.O., Bult C, Fletcher C, Fujita M, Gariboldi M,
 RA Gustincich S., Hill D, Holmann M, Hume D.A., Kaniya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombereis P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Wittaker C., Wilting L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL: AK004114; BAB21177.1; -
 DR MGD; MGI:1891829; Rbx1.
 SQ SEQUENCE 122 AA; 13321 MW; 39736A8BD4DCB04F CRC64;

Alignment Scores:

Pred. No.: 1.55e-39 Length: 122
 Score: 416.00 Matches: 89
 Percent Similarity: 82.88% Conservative: 3
 Best Local Similarity: 80.18% Mismatches: 18
 Query Match: 43.24% Indels: 1
 DB: 11 Gaps: 0

US-09-914-324A-3 (1-508) x QY0105 (1-122)

QY 7 ATGGCGGAGGATGATGTGATACCCGAGCGGACCAACAGCGGCGGCGGCAAG 66

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Db      1 MetAlaAlaAlaMetAspValAspThrPro-AlaAlaProThrAlaAlaArgAlaAspSe 20
QY      67 CGCTTTAGAGTGAAGAAAGTGAATGCAGTACCCCTCGGCGCTGAGTATTTGTTGAT 126
Db      20 FAlaLeuLeuLeuLeuLeuSerGlyMetGlnTrpProSerGlyArgGlyThrLeuTrpLeu11 40
QY      127 AACTGTGCATCTCGAGAACCACTTATGATCTTTGCATGAGATGTCAAGCTAACCGAG 186
Db      40 ethrValProSerAlaGlyThrThrLeuTrpIlePheValSerAsnValArgProThrAr 60
QY      187 GGGTCCGCTACTTTCAGAGAGAGTCTGCGATGGGAGTGTGTAACCATGCTTTTAC 246
Db      60 gArgGlnLeuLeuProLysSerValArgLeuHisLeuLeuSerAlaThrMetLeuPhe11 80
QY      247 TTCACATGATCTCTCGCTGCTGCTCAAAACAGCAGGTGTGTCCATTGGACACAGAGAG 306
Db      80 eSerThrAlaSerLeuAspGlySerLysArgGlyArgValArgTrpThrThrGluSe 100
QY      307 TGGGAATTCGAAAGTATGGGACACTAGGAAA 337
Db      100 rGlySerSerArgSerMetGlyIleArgLys 110

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RESULT 4

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077367 PRELIMINARY: PRT: 107 AA.
ID 077367
AC 077367;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative ring finger protein.
GN MAL3P6_28.
OC Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=35329;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RC MEDLINE=99376085; PubMed=10448855;
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
RA Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA Horrocks P., Jagsels K., Jassal B., Kyes S., McLean J., Moule S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
RA Rutter S., Skelton J., Squares R., Squares S., Sulten J.E.,
RA Whitehead S., Woodward C., Barrett B.G.;
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
RT falciparum."
RL Nature 400:532-538(1999).
DR EMBL; Z98551; CAB1123.3; -.
DR PIR; T18513; T18513.
DR InterPro; IPR001841; ZnF_ring.
DR Pfam; PF00097; zf-C3HC4_1.
DR SMART; SMC0184; RING; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR QY 107 AA; 12419 MW; CS63432A60F20262 CRC64;
SQ SEQUENCE 107 AA; 12419 MW; CS63432A60F20262 CRC64;

```

Alignment Scores:

```

Pred. No.: 4.2e-35 Length: 107
Score: 378.00 Matches: 64
Percent Similarity: 75.00% Conservative: 5
Best Local Similarity: 69.57% Mismatches: 15
Query Match: 39.29% Indels: 8
DB: Gaps: 1

```

US-09-914-324A-3 (1-508) x 077367 (1-107)

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QY 70 TTGAAGTGAAGAAAGTGAATGCAGTACCCCTCGGCGCTGAGTATTTGTTGATTAAC 129
Db 13 PheylsleHisLysTrpSerAlaValAlaAlaTrpSerTrpAspIleSerValAspAsn 32
QY 130 TGTGCATCTGCAGGAACCACTTATGATCTTTGCATGAGATGTCAAGCT 180

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Db      33 CysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaLysThr 52
QY      181 -----AACGAGCGTCCGCTACTTTCAGAAAGTGTACTGTGCAGGGGA 225
Db      53 AspHisGluAsnAspLysAspLysLysIleAspLysGluGlyCysThrValAlaTrpGly 72
QY      226 GTCTGTAACTGATCTTTTCACTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 285
Db      73 ValCysAsnHisAlaPheHisIleuHisCysIleSerArgTrpIleLysAlaArgGlnVal 92
QY      286 TGTTCATTGGAACAACAGAGAGTGGGAATTCGAAAG 321
Db      93 CysProLeuAspAsnThrThrTrpGluPheGlnLys 104

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RESULT 5

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09FTN1 PRELIMINARY: PRT: 97 AA.
ID 09FTN1
AC 09FTN1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P0005A05.18 protein (P0482C06.1 protein).
DE P0005A05.18 OR P0482C06.1.
GN Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipondare;
RC Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipondare (GA3) genomic DNA, chromosome 1, PAC
RT clone: P0005A05."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002863; BAB16914.1; -.
DR EMBL; AP002865; BAB78605.1; -.
DR Gramene; Q9FTN1; -.
SQ SEQUENCE 97 AA; 10329 MW; FDD1CE73EDBA579 CRC64;

```

Alignment Scores:

```

Pred. No.: 1.09e-27 Length: 97
Score: 314.50 Matches: 59
Percent Similarity: 75.29% Conservative: 5
Best Local Similarity: 69.41% Mismatches: 4
Query Match: 32.69% Indels: 17
DB: Gaps: 2

```

US-09-914-324A-3 (1-508) x 09FTN1 (1-97)

```

QY 22 GATGTGATACCCCG-----AACGCGACCCAC 48
Db 4 AspIleAsnAlaProProProProAlaProAlaProAlaGlyAlaGlyGlySerSer 23
QY 49 AGCGCGCGGCGC-----AAGAAGCGCTTTGAAAGTGAAGTGAAT 90
Db 24 SerAlaIleGlyProSerSerArgLysProAsnLysArgPheGlnIleLysLysTrpAsn 43
QY 91 GCATGAGCCCTCTGCGCTGCGATGATGTTGATTAAGTGCATGCTGAGGAACAC 150
Db 44 AlaValAlaLeuTrpAlaTrpAspIleValAlaAspAsnCysAlaIleCysArgAsnHis 63
QY 151 ATTATGATCTTTGCATGAGATGTCAAGCTAACGAGCGTCCGCTACTTGAAGAGTGT 210
Db 64 IleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCys 83

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RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Bertram B., Carlson J.W., Celniker S.E.,
 RA Clump M., Drysdale R., Emmert D., Friese G., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Milburn G., Richter J., Russo S.,
 RA Seattle S.M.J., Smith E., Shu S., Smutnick F., Whitfield B.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
 RT "Annotation of Drosophila melanogaster genome."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.,
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champagne M., Chavez C., Dorsett V., Dreanek D., Farfan D., Friese E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Munoz J., Paclob U., Paragas V., Park S.,
 RA Patel S., Phouenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.,
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003825; AAF58633.2; -;
 DR EMBL; AY113544; AAM29549.1; -;
 DR FLYBase; FBgn003641; CG8998.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 SQ SEQUENCE 113 AA; 13101 MW; 41F16639A2EC1252 CRC64;

Alignment Scores:
 Pred. No.: 3.58e-24 Length: 113
 Score: 284.50 Matches: 48
 Percent Similarity: 63.46% Conservative: 18
 Best Local Similarity: 46.15% Mismatches: 35
 Query Match: 29.57% Indels: 3
 DB: Gaps: 2

US-09-914-324a-3 (1-508) x Q9V607 (1-113)

QY 25 GTGATATCCCGGCGCGCACCC--AACAGCGCGCGCGCAAGAGCGCTTGAAGTGA 81
 DB 9 ValAspArgProThrAspAspGlyAspAlaGlyLysProGluLysMetPheThrLeuLys 28
 QY 82 AAGTGAATGACAGTATGAGCCCTCTGAGGCTGGAATATGTTGTTGATTAATGATGCTG 141
 DB 29 LysTyrPheAsnAlaValAlaMetTyrPserTyrPaspValGluLysAspIleCysAlaIleCys 48
 QY 142 AGGACACCACTATGATGCTTTGATGATGATGATGATGATGATGATGATGATGATGATG 198
 DB 49 ArgValAlaGlnValMetAspSerCysLeuArgCysGlnAlaAspAsnLysArgAspValMet 68
 QY 199 ---TCAGAGAGTGTACTGTGCGCATGGGAGTCTGTATACCATGCTTTTCACTTCG 255
 DB 69 GlyArgGlnAspCysValAlaValTyrGlyGluCysAsnHisSerPheHisLscysCys 88
 QY 256 ATCTCTGCGTGCCTCAAAACACGACAGAGTGTGCTTGCATGACACAGAGAGTGGAAATC 315
 DB 89 MetSerLeuTyrValLysGlnAsnAsnArgCysProLeuGlyGlnGlnGlnTyrPserIle 108
 QY 316 CAAAGTATGAG 327
 DB 109 GlnArgMetGly 112
 RESULT 8
 P91404 PRELIMINARY; PRT; 112 AA.
 ID P91404
 AC P91404;

DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE R10A10.2 protein.
 GN R10A10.2
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten N., Laister P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
 RA Smaildon N., Smith A., Sornhammet E., Staden R., Sulston J.,
 RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterson R.,
 RA Watson A., Weinstock L., Wilkinson-Sprat J., Wohlman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans."
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wamsley, P., Bradshaw H.;
 RT "The sequence of C. elegans cosmid R10A10."
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterson R.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U80449; AB37826.1; -;
 DR PIR; T29620; T29620.
 DR HSSP; P28990; ICHC.
 DR WormPep; R10A10.2; CE12670.
 DR InterPro; IPR001526; IY6 UPAR.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SMO0184; RING; 1.
 DR PROSITE; PS00983; IY6 UPAR; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 SQ SEQUENCE 112 AA; 12871 MW; 8F797E10FB701092 CRC64;

Alignment Scores:
 Pred. No.: 5.2e-22 Length: 112
 Score: 266.00 Matches: 45
 Percent Similarity: 59.63% Conservative: 20
 Best Local Similarity: 41.28% Mismatches: 32
 Query Match: 27.65% Indels: 12
 DB: Gaps: 2

US-09-914-324a-3 (1-508) x P91404 (1-112)

QY 7 ATGGCGGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 66
 DB 1 MetAsnAsnSerSerAsnAlaAspSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 20
 QY 67 CGC-----TTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 102
 DB 21 ThrAlaAsnProSerGlnSerArgProPheValLeuLysLysTyrPaspAlaLeuAlaVal 40
 QY 103 TGGCGCTGAGATATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 162
 DB 41 TrpAlaTyrPaspValGluCysAspPheCysAlaIleCysArgValHisLeuMetGlnGlu 60
 QY 163 TGCATAGATGCTCAAGCTAACACGAGCGCTCCGCTACTTATGAGAAGTGTATGTCATG 222

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Db      61 CyeLeuArgCysGln-----SerGluProSerAlaGluCysTyrValValTyrP 76
QY      223 GGAGTGTGAACCACTGTTTCACTTCACCTGCATCTCGCTGAGCTCAAAACACACAG 282
      77 G1yAspCysAsnHisSerPheHisH1sCysCysMetThrGlnTyrP1leArgGlnAsnHis 96
QY      283 GTGTGTCCATTCGACACACAGAGAGTGG 309
      97 ArgCysProLeuGlyCysGlnTyrP1leAspTyrP 105

RESULT 9
ID 0940X6 PRELIMINARY; PRT; 84 AA.
AC 0940X6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Anaphase promoting complex subunit 11.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid1; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Okresz L.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AY052402; AAL13436.1;
DR InterPro; IPR01841; Znf_Ring.
DR Pfam; PF00097; Zf-C3HC4; 1.
DR SMART; SMO0184; RING; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KM Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 84 AA; 9766 MW; 049678PED5882D6 CRC64;

Alignment Scores:
Pred. No.: 1.75e-15 Length: 84
Score: 210.00 Matches: 34
Percent Similarity: 59.09% Conservative: 18
Best Local Similarity: 38.64% Mismatches: 28
Query Match: 21.83% Indels: 8
DB: Gaps: 3

US-09-914-324A-3 (1-508) x 0940X6 (1-84)
QY 67 CGCTTTGAAGTGAAGTGAATGCAATGACCTCTGGGCTGGATATTGGTTGAT 126
      2 LysValIysIleLeuArgTyrP1leAlaValAlaSerTyrP1leArgPalaGlnAspGlu 21
QY 127 AACTGTGCATCTCGCTGAGACACACATTGTGATCTTTGCATGATGCAAGTAAACAG 166
      22 ThrCysGlyIleCysArgMetAlaPheAspGlyCysCysProAspCysLys----- 38
Db      187 GCGTCCGCTACTTCAGAGAGTGTACTGTCGATGGAGAGTGTAAACATGCTTTTCA 246
QY 39 -----LeuProGlyAspAspCysProLeuIleTyrP1leCysAsnHisAlaPheHis 56
      247 TTCACCTGCATCTCGCTGCTC-----AAACACACACAGGCG-----TGTCCATTGGAC 297
Db      57 LeuHisCysIleLeuIleTyrPalaAsnSerGlnHisAlaHisCysProMetCys 76
QY 298 AACAGAGATGGATCCCAAG 321
      77 ArgArgGlnTyrP1leGlnPheLysGlu 84

RESULT 10
ID 08H306 PRELIMINARY; PRT; 84 AA.
AC 08H306;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

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DE Putative anaphase promoting complex subunit 11.
OS Oryza sativa (Japanese cultivated rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriacoidae; Oryzaceae; Oryza.
OC NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (Gh3) genomic DNA, chromosome 7, PAC
RT clone: p0710f09."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005325; BAC21540.1;
DR InterPro; IPR01841; Znf_Ring.
DR Pfam; PF00097; Zf-C3HC4; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 84 AA; 9676 MW; 5CF99B1E32D5E09A CRC64;

Alignment Scores:
Pred. No.: 4.41e-14 Length: 84
Score: 198.00 Matches: 30
Percent Similarity: 57.47% Conservative: 20
Best Local Similarity: 34.48% Mismatches: 29
Query Match: 20.58% Indels: 8
DB: Gaps: 2

US-09-914-324A-3 (1-508) x 08H306 (1-84)
QY 67 CGCTTTGAAGTGAAGTGAATGCAATGACCTCTGGGCTGGATATTGGTTGAT 126
      2 LysValIysIleLeuArgTyrP1leGlyValAlaSerTyrP1leArgPalaGlnAspGlu 21
QY 127 AACTGTGCATCTCGCTGAGACACACATTGTGATCTTTGCATGATGCAAGTAAACAG 166
      22 ThrCysGlyIleCysArgMetAlaPheAspGlyCysCysProAspCysLys----- 38
Db      187 GCGTCCGCTACTTCAGAGAGTGTACTGTCGATGGAGAGTGTAAACATGCTTTTCA 246
QY 39 -----PheProGlyAspAspCysProLeuIleTyrP1leGlySerCysAsnHisAlaPheHis 56
      247 TTCACCTGCATCTCGCTGCTC-----CAAGTGTTCATTGGAC 297
Db      57 LeuHisCysIleLeuIleTyrPalaAsnSerGlnHisAlaHisCysProMetCys 76
QY 298 AACAGAGATGGATCCCA 318
      77 ArgArgGlnTyrP1leGlnPheLys 83

RESULT 11
ID 09VLJ5 PRELIMINARY; PRT; 85 AA.
AC 09VLJ5; GSNLJ4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Cg18042 protein (putative APC11 anaphase-promoting complex
DE subunit).
GN IMG OR Cg18042.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachytera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Berkely;
RA MEDLINE=20156006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anandides P.G., Scherter S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

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RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abul J.F., Agbayan A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhattacharya D., Bolshakov S.,
 RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dopp L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dudin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hoshin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko F., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milhina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclebo J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reiter K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spirdling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.O.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RT Science 287:2185-2195 (2000).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Celinker S.E., Adams M.D., Kronmiller B., Man K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amaratilake P.G., Brandon R.C., Rogers Y.,
 RA Banton J., An H., Baldwin D., Banton J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorssett V., Dopp L.E., Doyle C., Dresnek D., Farrant D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hoshin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nuno J.,
 RA Paclebo J., Paragay V., Park S., Patel S., Pfeiffer B., Scheeler F.,
 RA Shounenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
 RT "Sequencing of *Drosophila melanogaster* genome."
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
 RA Mista S., Crosby N.A., Mathews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradsky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Bernan B., Carlson J.W., Celinker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
 RT "Annotation of *Drosophila melanogaster* genome."
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]

RP SEQUENCE FROM N.A.
 RA Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter J.C.,
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Flybase,
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Taylor C.A., Shitras A.D.;

RT "Cell cycle arrest and apoptosis in lemming mutants of *Drosophila*
 RT melanogaster."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RA EMBL: AE003621; AAF52694.2;
 DR EMBL: AJ251510; CAB63945.1;
 DR Flybase: FBgn0029004; lmg.
 DR InterPro: IPR001841; Znf_ring.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 SQ SEQUENCE 85 AA; 9859 MW; 01EF449D32BEDBA2 CRC64;

Alignment Scores:
 Pred. No.: 5,79e-14 Length: 85
 Score: 197.00 Matches: 31
 Percent Similarity: 53.01% Conservative: 13
 Best Local Similarity: 37.35% Mismatches: 31
 Query Match: 20.48% Gaps: 2
 DB: 5

US-09-914-324a-3 (1-508) x Q9VLT5 (1-85)

QY 76 GTGAAAAGTGAATGACATGACCCCTGGCGGATGTTGTGATTAATGATGCGC 135
 Db 5 ILeYsesttrphrglyvalAlahnrtpargrtptlAlasmbpoulsncysgly 24
 QY 136 ATCTGAGGAGACACATTAATGATCTTTGCATAGAAATGCAAGCTAACCGGCGTCCGT 195
 Db 25 ILeCyArgrYsestserhegusesthrCysproglucys-----Alaleu 39
 QY 196 ACTTCAGAGAGTGTACTGTGCGATGGAGAGTGTACCAATGCTTTGACTTCACGTCG 255
 Db 40 ProGlyAspAspCysAsprouleuValtrpGlyvalCyssestheCysphenstheCys 59
 QY 256 ATCTCGCGTGGCTGCTCAAAACACAGCAGCTG-----TGTCATTGGAACAACAGAGAG 306
 Db 60 ILevallystrpneuhsenleuGlnProleuAsnlyGlnCysretwetCysarginsr 79
 QY 307 TGGGAATTC 315
 Db 80 TrpLysphe 82

RESULT 12
 ID 081CC8 PRELIMINARY; PRT; 89 AA.
 AC 081CC8;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
 DE Anaphase-promoting complex subunit, putative.
 GN Ml6p1.184.
 OS Plasmidium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmidium.
 OX NCBI_TaxID=36329;

RP SEQUENCE FROM N.A.
 RA Cherevach I., Davis P., Goodhead I., Stevens K., Mungall K.,
 RA Berriman M., Bain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
 RA Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrett B.,
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RA EMBL: AL844505; CAD50514.1;
 DR InterPro: IPR001841; Znf_ring.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 SQ SEQUENCE 89 AA; 10211 MW; 9874B3D9583BA23D CRC64;

Alignment Scores:
 Pred. No.: 1.38e-08 Length: 89
 Score: 151.00 Matches: 28
 Percent Similarity: 52.38% Conservative: 16
 Best Local Similarity: 33.33% Mismatches: 32
 Query Match: 15.70% Indels: 8
 DB: 5 Gaps: 4

US-09-914-324a-3 (1-508) x 081CC8 (1-89)


```
QY 76 GTGAAAGAGTGAATGAGTACGCTGCGCTGG---GATATTGGTTGATAC--- 129
DB 6 ValValArgTleHtSalValAlaArgTlPylleGlySerThrIleAspSerVal 25
QY 130 TGTGCATCTGCGAGGACCAACATTATGATCTTTCATAGATATGCAAGCTAACCGAGG 189
DB 26 CysAlaIleCysAsnSerSerLeuGluAsnThrCysThrThrCysMet----- 41
QY 190 TCOCCTCTTCAGAGAGTGTACTGTGCGATGGGGGTCTGTACACATGCTTTCACTTC 249
DB 42 ---ArgProGlyAsnGlyCysProProAlaPheIlylCysGlyHisIlePheIleu 60
QY 250 CACTGCATCTCTGCTGCTGCTGCTCAAAACACGACAGTG---TGTCCATTGACACAGAGAG 306
DB 61 HicCysMetGluLysTlPylleGlyGlnAsnLysLeuThrCysProCysCysArgAlaAsp 80
QY 307 TGGGAATTCCAA 318
DB 81 TrpTyrTyrGlu 84

RESULT 13
Q20052 PRELIMINARY; PRT; 135 AA.
AC Q20052;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE F35G12.9 protein.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditioidea;
OC Rhabditidae; Pelodietinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Chui C.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=99069613; PubMed=9851916;
RX none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; Z46242; CA86328.1; -.
DR PIR; T21802; T21802.
DR WormPep; F35G12.9; CE00978.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SMO0184; RING; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KM Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 135 AA; 15512 MW; 1CC8BAF1AB67157 CRC64;

Alignment Scores:
Pred. No.: 4.94e-08 Length: 135
Score: 146.50 Matches: 28
Percent Similarity: 45.24% Conservative: 10
Best Local Similarity: 33.33% Mismatches: 35
Query Match: 15.23% Indels: 11
Gaps: 3

US-09-914-324A-3 (1-508) x Q20052 (1-135)
QY 76 GTGAAAGAGTGAATGAGTACGCTGCGCTGG---GATATTGGTTGATAC--- 132
DB 53 ValLysLysLeuHtSalValAlaArgTlPylleGlySerThrIleAspThrCys 72
QY 133 GCCATCTGCGAGGACCAACATTATGATCTTTCATAGATATGCAAGCTAACCGAGCTCC 192
DB 73 GlyIleCysArgMetGluPheGluSerAlaCys-----AsnMetCysLys 87
```

```
QY 193 GCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACGATCTTTCACCTTCAC 252
DB 88 PheProGlyAspArgPysProLeuValLeuGlyIleCysArgHisAlaPheHisArgHis 107
QY 253 TGCATCTGCGCTGGCTC-----AAACACGACAGCGTGTGTCATTGGAC 297
DB 108 CysIleAspLysTlPylleAlaAlaProThrAsnGlnProAlaGlnCysProLeuCys 127
QY 298 AACAGAGAGTG 309
DB 128 ArgGlnAspTrp 131

RESULT 14
Q9M9L0 PRELIMINARY; PRT; 57 AA.
ID Q9M9L0;
AC Q9M9L0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE F10A16.17 protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidops.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
RA Roming C.M., Koo H., Fujii C.Y., Utechtack T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL "Arabidopsis thaliana chromosome III BAC F10A16 genomic sequence."
Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AC012393; AAF26089.1; -.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SMO0184; RING; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KM Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 57 AA; 6580 MW; 504C753B7B745C74 CRC64;

Alignment Scores:
Pred. No.: 1.91e-07 Length: 57
Score: 141.00 Matches: 23
Percent Similarity: 62.50% Conservative: 12
Best Local Similarity: 41.07% Mismatches: 13
Query Match: 14.66% Indels: 8
Gaps: 3

US-09-914-324A-3 (1-508) x Q9M9L0 (1-57)
QY 163 TGCATGAGTGTGCAAGCTAACCGAGCGTCCGCTACTTCAGAGAGTGTACTGTGCGATCG 222
DB 7 CysProAspCysLys-----LeuProGlyAspArgPysProLeuIleTrp 21
QY 223 GGAGTGTGAACCATGCTTTCATCTCCATGCAATCTCTCGCTGCTC-----AAAACA 276
DB 22 GlyAlaCysAsnHisAlaPheHisLeuHisCysIleLeuLysTlPylleValAsnSerGlnThr 41
QY 277 CCACAGAGTG---TGTCCATTGACACAGAGAGTGGAATTCCAAAG 321
DB 42 SerGlnAlaHisCysProMetCysArgArgGluTrpGlnPheLysGlu 57

RESULT 15
ID Q12157 PRELIMINARY; PRT; 165 AA.
ID Q12157;
AC Q12157;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chromosome IV reading frame ORF YD1008W.
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 25, 2004, 09:32:07 ; Search time 21 seconds

(without alignments)
494.699 Million cell updates/sec

Title: US-09-914-324a-1

Perfect score: 616
Sequence: 1 MAAMDVDTPTSGTNSGAGKK.....KTRQVCPIDNREMEFQKXGH 108Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96151526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR78:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	616	100.0	108	2	T51146
2	510	82.8	136	2	T13388
3	499	81.0	115	2	T47341
4	493	80.0	110	2	T27823
5	469	76.1	107	2	T38310
6	385	62.5	121	2	S66830
7	378	61.4	166	2	T18513
8	266	43.2	112	2	T29620
9	164.5	26.7	94	2	T29652
10	146.5	23.8	135	2	T21802
11	136	22.1	165	2	S52511
12	132.5	21.5	99	2	S90113
13	116.5	18.9	2160	2	T20241
14	104	16.9	349	2	T06680
15	102.5	16.6	249	2	C96775
16	102	16.6	210	2	T45654
17	100	16.2	676	2	T47637
18	97	15.7	159	2	T48209
19	97	15.7	327	2	D86474
20	96	15.6	332	2	D86448
21	95.5	15.5	441	2	F71425
22	95	15.4	253	2	T06113
23	95	15.4	322	2	H85474
24	95	15.4	336	2	T28358
25	95	15.4	362	2	T51464
26	95	15.4	530	2	T50499
27	92	14.9	689	2	F84811
28	92	14.9	185	2	T51844
29	91.5	14.9	190	2	T51859

30	91.5	14.9	496	2	B96674	hypothetical prote
31	91.5	14.9	571	2	T40911	probable PHD-type
32	91	14.8	530	2	T28366	ORF MSV205 tryptop
33	90.5	14.7	677	2	T39713	zinc finger protei
34	90	14.6	213	2	T14811	hypothetical prote
35	90	14.6	532	2	T49467	related to Cobl-1n
36	90	14.6	1208	2	T05077	hypothetical prote
37	89.5	14.5	202	2	T06621	hypothetical prote
38	89.5	14.5	624	2	T01585	probable RING zinc
39	89	14.4	357	2	E85092	hypothetical prote
40	89	14.4	456	2	T19377	hypothetical prote
41	88.5	14.4	336	2	A86405	probable RING zinc
42	88.5	14.4	524	2	F96572	protein F12M5.10
43	88	14.3	141	2	S15788	intermediate early
44	88	14.3	161	2	E88541	protein ZK637.14 l
45	88	14.3	200	2	T41745	RING-H2 finger pro

ALIGNMENTS

RESULT 1

T51146
ring-box protein 1 [imported] - human

C:Species: Homo sapiens (man)

C>Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000

C:Accession: T51146

R:Kamura, T., Keopp, D.M., Conrad, M.N., Skowrya, D., Moreland, R.J., Iliopoulos, O., Le

Science 284, 657-661, 1999

A:Title: Rbx1, a component of the VHL tumor suppressor complex and SCF ubiquitin ligase.

A:Reference number: 225317, PMID:9234320, PMID:10213691

A:Accession: T51146

A>Status: Preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-108 <KAM>

A:Cross-references: EMBL:AF140598; PIDN:AA029715.1

C:Genetics:

A:Gene: RBX1

Query Match 100.0%; Score 616; DB 2; Length 108;

Best local similarity 100.0%; Pred. No. 1.5e-58;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MAAMDVDTPTSGTNSGAGKKRFEYKKNVAVLWAMDIVDNCAICRNHIMDICEQANG 60

Db 1 MAAMDVDTPTSGTNSGAGKKRFEYKKNVAVLWAMDIVDNCAICRNHIMDICEQANG 60

Cy 61 ASATSECTVAVGVCNHAFFHCISRRLKTRQVCPIDNREMEFQKXGH 108

Db 61 ASATSECTVAVGVCNHAFFHCISRRLKTRQVCPIDNREMEFQKXGH 108

RESULT 2

T13388
hypothetical protein 115C2.11 - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C:Accession: T13388

R:Salles, C., Valenti, P., Darlamitso, A., Henderson, N., Campbell, L., Glover, D.

submitted to the EMBL data library, May 1999

A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.

A:Reference number: 21765

A:Accession: T13388

A>Status: Preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-136 <CAT>

A:Cross-references: EMBL:AL031581; PIDN:CAA20888.1

C:Genetics:

A:Cross-references: Flybase:FBgn0020381

A:Introns: 64/7

A>Note: EG:115C2.11

Query Match 82.8%; Score 510; DB 2; Length 136;

A:Cross-references: SGD:S0005493
 A:Map position: 15L
 A>Note: YOL133w
 C:Superfamily: yeast hypothetical protein YOL133w; RING finger homology

Query Match 62.5%; Score 385; DB 2; Length 121;
 Best Local Similarity 56.6%; Pred. No. 6, 9e-34;
 Matches 64; Conservative 10; Mismatches 29; Indels 10; Gaps 1;

5 MDVDPSTGNSGAG-----KKRFVKKNNAVALMAMDIVVNDCAICRNHIMDL 54
 8 MDVDEDSQNIAGSSNQAPVETKKRFEIKKMTAVAFMSQDIAYDNCALCRNHIMBPI 67

QY 55 ECGANQASATSECTVAMGVCHAFPHICISRMILKTRQVCPIDNREMEFQKG 107
 DB 68 ECGPKAMTDIDNECVAMGVCHAFPHILCINIKTRKDCPLDNQPMQLARCG 120

RESULT 7
 T18513
 hypothetical protein C0845c - malaria parasite (Plasmodium falciparum)

C:Species: Plasmodium falciparum
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
 C:Accession: T18513

R:Lawson, D.; Bowman, S.; Barrell, B.
 submitted to the EMBL Data Library, August 1997

A:Reference number: Z18935
 A:Accession: T18513
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-166 <LAW>
 A:Cross-references: EMBL:Z98551; PIDN:CAB1123.2

C:Genetics:
 A:Map position: 3
 A:introns: 19/1
 A>Note: C0845c

Query Match 61.4%; Score 378; DB 2; Length 166;
 Best Local Similarity 59.6%; Pred. No. 5, 2e-33;
 Matches 64; Conservative 5; Mismatches 15; Indels 8; Gaps 1;

QY 22 FEVKNNNAVALMAMDIVVNDCAICRNHIMDLCEGCA-----NQASATSECTVAMG 73
 DB 72 FKHKMSAVAAWMDISVNDCAICRNHIMDLCEGCAKTTDENDKRIKREGCTVAMG 131

QY 74 VCNHAFPHICISRMILKTRQVCPIDNREMEFQK 105
 DB 132 VCNHAFPHICISRMILKTRQVCPIDNREMEFQK 163

RESULT 8
 T29620
 hypothetical protein R10A10.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Aug-2002
 C:Accession: T29620

R:Wamsley, P.; Bradshaw, H.
 submitted to the EMBL Data Library, November 1996

A:Description: The sequence of C. elegans cosmid R10A10.
 A:Reference number: Z20653

A:Accession: T29620
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-112 <WAM>
 A:Cross-references: EMBL:U80449; PIDN:AAB37826.1; GSPDB:GN00019; CESP:R10A10.2

C:Genetics:
 A:Gene: CESP:R10A10.2
 A:Map position: 1
 A:introns: 17/2; 59/1

C:Superfamily: yeast hypothetical protein YOL133w; RING finger homology
 Query Match 43.2%; Score 266; DB 2; Length 112;

Best Local Similarity 41.3%; Pred. No. 3e-21;
 Matches 45; Conservative 20; Mismatches 32; Indels 12; Gaps 2;

QY 1 MAAMDVDPSTGNSGAGKKR-----FEVKNNNAVALMAMDIVVNDCAICRNHIMDL 52
 DB 1 MNSSNADSQEGSTAQKQKTANPSRPFLVKNNNAVALMAMDIVVNDCAICRNHIMB 60

QY 53 CIEGQANQASATSECTVAMGVCHAFPHICISRMILKTRQVCPIDNREMEFQKG 101
 DB 61 CLRCQ-----SEPSAECTVAMGDCNHSFHHCCMTQWIRONNRCPLOCQKW 105

RESULT 9
 T38652
 hypothetical protein SPAC343.03 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T38652

R:Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, August 1997

A:Reference number: Z21804
 A:Accession: T38652
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-94 <MDR>
 A:Cross-references: EMBL:AL109739; NID:e1534774; PIDN:CAB52266.1; GSPDB:GN00066; SPDB:SI

A:Experimental source: strain 972h; cosmid c343
 C:Genetics:
 A:Gene: SPDB:SPAC343.03
 A:Map position: 1
 A:introns: 7/1; 48/1

Query Match 26.7%; Score 164.5; DB 2; Length 94;
 Best Local Similarity 33.7%; Pred. No. 1, 7e-10;
 Matches 28; Conservative 16; Mismatches 30; Indels 9; Gaps 3;

QY 21 FEVKNNNAVALMAMDIVVNDCAICRNHIMDLCEGQANQASATSECTVAMGVCHAF 79
 DB 2 KVKILRFHAIAMWTMDIPKDDVCGICRVPDGGCPCQ-----TSPGNCPTVMGCKHIF 56

QY 80 HFHCISRMILKTRQVCPIDNREMEFQK 99
 DB 57 HAHCIQWMLATSSGSGGCPMDRQ 79

RESULT 10
 T21802
 hypothetical protein F35G12.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Aug-2002
 C:Accession: T21802

R:Chui, C.
 submitted to the EMBL Data Library, October 1994

A:Reference number: Z19473
 A:Accession: T21802
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-135 <WIL>
 A:Cross-references: EMBL:Z46242; PIDN:CAA86328.1; GSPDB:GN00021; CESP:F35G12.9

A:Experimental source: clone F35G12
 C:Genetics:
 A:Gene: CESP:F35G12.9
 A:Map position: 3

A:introns: 33/3; 57/3
 C:Superfamily: yeast hypothetical protein YOL133w; RING finger homology

F:68-133/Domain: RING finger homology <RXN>

Query Match 23.8%; Score 146.5; DB 2; Length 135;
 Best Local Similarity 33.3%; Pred. No. 2e-08;
 Matches 28; Conservative 10; Mismatches 35; Indels 11; Gaps 3;

QY 24 VKKNNAVALMAMDIVVNDCAICRNHIMDLCEGQANQASATSECTVAMGVCHAFPH 82

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 25, 2004, 09:24:27 ; Search time 55 Seconds
(without alignments)
554.821 Million cell updates/sec

Title: US-09-914-324A-1

Perfect score: 616
Sequence: 1 MAAMDVDPSTGNTSGAGKK.....KTRQVCPDNRNEMFQXGH 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp19806:*
2: geneseqp19806:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20025:*
6: geneseqp20036:*
7: geneseqp20036:*
8: geneseqp20046:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	616	100.0	108	3 AAB19160	AAB19160 Amino aci
2	616	100.0	108	3 AAB08813	AAB08813 A human c
3	616	100.0	108	3 AAG03890	AAG03890 Human sec
4	616	100.0	108	4 AAB47559	AAB47559 ROC1. 1/2
5	616	100.0	108	5 AAE24620	AAE24620 Human RIN
6	616	100.0	108	7 ADC02481	ADC02481 RING fing
7	534	86.7	108	4 ABB68080	ABB68080 Drosophil
8	514.5	83.5	118	3 AAG23004	AAG23004 Arabidops
9	511	83.0	109	3 AAG23005	AAG23005 Arabidops
10	400.5	65.0	122	4 ABB66109	ABB66109 Drosophil
11	385	62.5	121	3 AAB08814	AAB08814 A yeast c
12	323	52.4	57	3 AAB41007	AAB41007 Human ORF
13	292	47.4	113	3 AAY06492	AAY06492 Human sen
14	292	47.4	113	3 AAB43295	AAB43295 Human ORF
15	292	47.4	118	4 AAU15873	AAU15873 Human nov
16	292	47.4	118	6 AAB05492	AAB05492 Human nov
17	292	47.4	131	4 AAU16332	AAU16332 Human nov
18	292	47.4	131	6 AAB05491	AAB05491 Human nov
19	291	47.2	113	2 AAY06509	AAY06509 Human sen
20	290.5	47.2	113	2 AAY06491	AAY06491 Mouse sen
21	290.5	47.2	113	3 AAB19161	AAB19161 Amino aci
22	287	46.6	113	4 AAB47600	AAB47600 ROC2. 1/2
23	287	46.6	113	5 AAB24621	AAB24621 Human RIN
24	287	46.6	113	7 ADC02483	ADC02483 RING fing
25	285	46.3	113	2 AAY06508	AAY06508 Human sen

26	283	45.9	113	2 AAY06500	AAY06500 Human sen
27	283	45.9	113	2 AAY06501	AAY06501 Human sen
28	282	45.8	113	2 AAY06496	AAY06496 Human sen
29	282	45.8	113	2 AAY06503	AAY06503 Human sen
30	282	45.8	113	2 AAY06502	AAY06502 Human sen
31	282	45.8	113	2 AAY06506	AAY06506 Human sen
32	282	45.8	113	2 AAY06495	AAY06495 Human sen
33	282	45.8	113	2 AAY06499	AAY06499 Human sen
34	282	45.8	113	2 AAY06498	AAY06498 Human sen
35	282	45.8	113	2 AAY06505	AAY06505 Human sen
36	274	44.5	113	2 AAY06504	AAY06504 Human sen
37	272	44.2	113	2 AAY06497	AAY06497 Human sen
38	272	44.2	113	2 AAY06507	AAY06507 Human sen
39	235	38.1	97	2 AAY06494	AAY06494 Human sen
40	235	38.1	97	3 AAB43284	AAB43284 Human ORF
41	213	34.6	88	3 AAB58912	AAB58912 Breast an
42	213	34.6	88	4 ABB12308	ABB12308 Human HSP
43	213	34.6	88	4 AAM79609	AAM79609 Human pro
44	213	34.6	91	5 ABB41805	ABB41805 Human ova
45	213	34.6	105	4 AAU16321	AAU16321 Human nov

ALIGNMENTS

RESULT 1
AAB19160 ID AAB19160 standard; protein; 108 AA.
XX
AC AAB19160;
XX
DT 19-FEB-2001 (first entry)
XX
DE Amino acid sequence of human ring finger protein ROC1.
XX
KW ROC1; ROC2; cullin; ring finger protein; APC1; APC complex; SCF pathway;
KW cullin dependent ubiquitin ligase; CDK inhibitor Sic1 degradation;
KW tumour.
XX
OS Homo sapiens.
XX
PN MO200058472-A2.
PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000MO-US008592.
XX
PR 31-MAR-1999; 99US-0127261P.
PR 22-NOV-1999; 99US-0166927P.
XX
PA (UNNC-) UNIV NORTH CAROLINA.
XX
PI Xiong Y, Ohta T;
XX
DR WP1; 2000-647235/62.
DR N-PSDB; AAA96882.
XX
PT Novel nucleic acid encoding cullin regulating ring finger proteins,
PT termed as ROC proteins similar to anaphase-promoting complex 11, for
PT therapeutic and diagnostic use.
XX
PS Claim 9; Fig 2A; 83pp; English.
XX
CC The present sequence represents a human ROC1 ring finger protein. The
CC specification also describes human ROC2. ROC1 and ROC2 are similar to
CC APC1, a subunit of the APC complex. The proteins stimulate cullin
CC dependent ubiquitin ligase activity. ROC1 functions in vivo as an
CC essential regulator of CDK inhibitor Sic1 degradation by the SCF
CC (undefined) pathway. ROC proteins are useful for screening bioactive
CC agents that interfere with the binding of ROC proteins with cullin
CC proteins. Pharmaceutical formulations comprising ROC proteins are useful
CC for diagnostic and therapeutic purposes, preferably for diagnosing and
CC treating tumours

XX Sequence 108 AA;

Query Match 100.0%; Score 616; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 3e-64;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAAMDVPSPGSGTSGAGKRFYVKKNAAVALMAMDIVDNCACRNHIMDLCTECQANQ 60
1 MAAAMDVPSPGSGTSGAGKRFYVKKNAAVALMAMDIVDNCACRNHIMDLCTECQANQ 60
DB 61 ASATSECTVAMGVCNNAHFHFCISRMLKTRQVCPLDNREWEFOKYGH 108

QY 61 ASATSECTVAMGVCNNAHFHFCISRMLKTRQVCPLDNREWEFOKYGH 108
DB 61 ASATSECTVAMGVCNNAHFHFCISRMLKTRQVCPLDNREWEFOKYGH 108

RESULT 2

AAB08813
ID AAB08813 standard; protein; 108 AA.

XX AAB08813;

DT 02-JAN-2001 (first entry)

XX A human cullin-interacting RING-H2 finger protein (Rbx1).

XX Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;
XX tumour suppressor; carcinoma; Ring box associated carcinoma;
XX von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;
XX cerebellar hemangioblastoma; hemangioma; retinal angiomata;
XX pheochromocytomas.

XX Homo sapiens.

XX MO200050445-A1.

XX 31-AUG-2000.

XX 25-FEB-2000; 2000MO-US004838.

XX 26-FEB-1999; 99US-0121787P.

XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.

XX Conway JA, Conway RC, Kamura T;

XX WPI: 2000-572067/53.

XX N-PSDB; AAA74978.

XX Cullin interacting RING-H2 finger protein, a component of von Hippel-Lindau tumor suppressor complex and Skp1-Cdc53P-F-box protein (SCF) ubiquitin ligase, useful for diagnosing and treating Ring box protein associated carcinomas.

XX Claim 1; Page 34; 37pp; English.

XX The present sequence represents a human cullin-interacting RING-H2 finger protein (Ring box protein), designated Rbx1. The polypeptide is a tumour suppressor. Rbx1 is useful for diagnosing a predisposition of a patient to certain carcinomas. It is also useful for treating Ring box protein associated carcinomas or augmenting metabolically deficient system in animals. Rbx1 is also useful for evaluating the effectiveness of a therapeutic treatment for Ring box associated carcinomas. Rbx1 can be used to screen for agents which augment or inhibit the activity of other cullin-containing ubiquitin ligase and of the VHL (von Hippel-Lindau) complex containing ubiquitin ligase and of the VHL (von Hippel-Lindau) proteins to various sets of target proteins. Carcinomas which may be treated include renal carcinomas, cerebellar hemangioblastomas and hemangiomas, retinal angiomata and pheochromocytomas

XX Sequence 108 AA;

Query Match 100.0%; Score 616; DB 3; Length 108;

Best Local Similarity 100.0%; Pred. No. 3e-64;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAAMDVPSPGSGTSGAGKRFYVKKNAAVALMAMDIVDNCACRNHIMDLCTECQANQ 60
1 MAAAMDVPSPGSGTSGAGKRFYVKKNAAVALMAMDIVDNCACRNHIMDLCTECQANQ 60
DB 61 ASATSECTVAMGVCNNAHFHFCISRMLKTRQVCPLDNREWEFOKYGH 108

QY 61 ASATSECTVAMGVCNNAHFHFCISRMLKTRQVCPLDNREWEFOKYGH 108
DB 61 ASATSECTVAMGVCNNAHFHFCISRMLKTRQVCPLDNREWEFOKYGH 108

RESULT 3

AAG03890
ID AAG03890 standard; protein; 108 AA.

XX AAG03890;

DT 06-OCT-2000 (first entry)

XX Human secreted protein, SEQ ID NO: 7971.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000/2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (GENET) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI: 2000-500381/45.

XX N-PSDB; AAC03896.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 13; SEQ ID NO 7971; 71pp + Sequence Listing; English.

XX The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or poly(A)-RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors

XX Sequence 108 AA;

Query Match 100.0%; Score 616; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 3e-64;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAAMDVPSPGSGTSGAGKRFYVKKNAAVALMAMDIVDNCACRNHIMDLCTECQANQ 60
1 MAAAMDVPSPGSGTSGAGKRFYVKKNAAVALMAMDIVDNCACRNHIMDLCTECQANQ 60
DB 61 ASATSECTVAMGVCNNAHFHFCISRMLKTRQVCPLDNREWEFOKYGH 108

QY 61 ASATSECTVAMGVCNNAHFHFCISRMLKTRQVCPLDNREWEFOKYGH 108

Db 61 ASATSECTVAMGVGNHAFHFCISRWLKTRQVCPDLNREMEFQKXGH 108

RESULT 4

AA847599 standard; protein; 108 AA.

AA847599;

07-JAN-2002 (first entry)

ROCI.

Assay; ubiquitin ligase; tag1-ubiquitin; E1, E2;
Kw ubiquitin activating enzyme; ubiquitin conjugating enzyme; E3;
Kw ubiquitin ligase; ubiquitination modulator.

Unidentified.

W0200175145-A2.

11-OCT-2001.

03-APR-2001; 2001WO-US010906.

03-APR-2000; 2000US-00542497.

(RIGE-) RIGEL PHARM INC.

Issakani SD, Huang J, Sheung J, Pray TR;

WPI; 2001-626445/72.

Assaying ubiquitin ligase activity for identifying modulators of
ubiquitination, by combining ubiquitin, ubiquitin activating conjugating
enzyme, ubiquitin ligase and measuring amount of ubiquitin bound to the
ligase.

Example 1; Fig 11; 98pp; English.

The sequences given in AA847596-602 are proteins which may be used in the
method of the invention for assaying ubiquitin ligase activity. The
method comprises combining under conditions that favour ubiquitin ligase
activity, tag1-ubiquitin, E1 (ubiquitin activating enzyme), E2 (ubiquitin
conjugating enzyme) and E3 (ubiquitin ligase) and measuring the amount of
tag1-ubiquitin bound to the E3. The method is useful for assaying
ubiquitin ligase activity and ubiquitination enzyme activity which is
useful for identifying ubiquitination modulator. The method comprises
combining tag1-ubiquitin, the modulator, E1, E2 and tag2-E3 and measuring
the amount of tag1-ubiquitin bound to tag2-E3 or combining tag1-
ubiquitin, modulator, E1 and tag3-E2 and measuring the amount of tag1-
ubiquitin bound to tag3-E2. Ubiquitin ligase activity is measured
directly, eliminating the need for target proteins and subsequent
analysis such as separating ligated from unligated material in an SDS-
PAGE procedure. This allows multi-well array analysis and high throughput
screening techniques for modulators of ubiquitination activity. The
method also allows the analysis of many different combinations of E3
components and E2/E3 combinations without requiring prior identification
of specific target substrates. Ubiquitin is labeled, directly or
indirectly and this allows for easy and rapid detection and measurement
of ligated ubiquitin

Sequence 108 AA;

Query Match 100.0%; Score 616; DB 4; Length 108;

Best Local Similarity 100.0%; Pred. No. 3e-64; Indels 0; Gaps 0;

Matches 108; Conservative 0; Mismatches 0;

QY 1 MAAMADVTSGTNSGAGKRFYVKKNAYALWAMDIVDNCALCRNHIMDLCEIQANQ 60
1 MAAMADVTSGTNSGAGKRFYVKKNAYALWAMDIVDNCALCRNHIMDLCEIQANQ 60
Db

QY 61 ASATSECTVAMGVGNHAFHFCISRWLKTRQVCPDLNREMEFQKXGH 108
Db 61 ASATSECTVAMGVGNHAFHFCISRWLKTRQVCPDLNREMEFQKXGH 108

RESULT 5

AAE24620 standard; protein; 108 AA.

AAE24620;

22-OCT-2002 (first entry)

Human RING finger protein, ROCI.

Ubiquitin ligase; UL; tag1-ubiquitin; E1; ubiquitin-activating enzyme;
Kw E2; ubiquitin-conjugating enzyme/ubiquitin carrier protein; E3; human;
Kw RING finger protein.

Homo sapiens.

US2002042083-A1.

11-APR-2002.

03-APR-2001; 2001US-00826312.

03-APR-2000; 2000US-00542497.

(RIGE-) RIGEL PHARM INC.

Issakani SD, Huang J, Sheung J, Pray TR;

WPI; 2002-488718/52.

Assay for ubiquitin ligase activity, useful for identifying modulators,
by measuring binding of labeled ubiquitin to ubiquitin ligase.

Disclosure; Fig 11; 56pp; English.

The invention relates to an assay for ubiquitin ligase (UL) activity
which comprises incubating tag1-ubiquitin, E1 (ubiquitin-activating
enzyme), E2 (ubiquitin-conjugating enzyme/ubiquitin carrier protein) and
E3 (UL) and measuring the amount of tag1-ubiquitin bound to E3. The
method is particularly used to screen for modulators of UL activity. The
present sequence is human RING finger protein, ROCI

Sequence 108 AA;

Query Match 100.0%; Score 616; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 3e-64;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAMADVTSGTNSGAGKRFYVKKNAYALWAMDIVDNCALCRNHIMDLCEIQANQ 60
1 MAAMADVTSGTNSGAGKRFYVKKNAYALWAMDIVDNCALCRNHIMDLCEIQANQ 60
Db

QY 61 ASATSECTVAMGVGNHAFHFCISRWLKTRQVCPDLNREMEFQKXGH 108
61 ASATSECTVAMGVGNHAFHFCISRWLKTRQVCPDLNREMEFQKXGH 108
Db 61 ASATSECTVAMGVGNHAFHFCISRWLKTRQVCPDLNREMEFQKXGH 108

RESULT 6

ADC02481 standard; protein; 108 AA.

ADC02481;

18-DEC-2003 (first entry)

RING finger protein ROCI.

ubiquitin; Mdm2; p53; RING finger protein; ROCI.

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XX Unidentified.
OS
XX US2003104474-A1.
XX
XX
XX
XX 05-JUN-2003.
XX
XX
XX 26-MAR-2002; 2002US-00108767.
XX
XX 03-APR-2000; 2000US-00542487.
XX
XX 03-APR-2001; 2001US-00826312.
XX
XX 04-MAR-2002; 2002US-00091139.
XX
XX (ISSA/) ISSAKANI S D.
XX (HUAN/) HUANG J.
XX (SHEU/) SHEUNG J.
XX (PRAY/) PRAY T R.
XX
XX Iseakani SD, Huang J, Sheung J, Pray TR,
XX
XX WPI; 2003-787056/74.
XX
XX Assaying for candidate agent that modulates attachment of ubiquitin
XX moiety to Mdm2 protein comprises combining ubiquitin agent comprising
XX ubiquitin moiety, Mdm2 protein, and candidate agent.
XX
XX Disclosure; Fig 11; 96pp; English.
XX
XX The present sequence represents a method of assaying for a candidate
XX agent that modulates the attachment of a ubiquitin moiety to an Mdm2
XX protein. The method is useful for assaying for a candidate agent that
XX modulates the attachment of a ubiquitin moiety to an Mdm2 or p53 protein.
XX The present sequence represents the amino acid sequence of RING finger
XX protein ROC1.
XX
XX
XX Sequence 108 AA:
SQ
Query Match 100.0%; Score 616; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 3e-64;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAAMDVDPGSGTSGAGKGFVEYKKNVAVLWMDIVNCAICRNHMDLCIECOANQ 60
DB 1 MAAAMDVDPGSGTSGAGKGFVEYKKNVAVLWMDIVNCAICRNHMDLCIECOANQ 60
QY 61 ASATSECTVAMGVGNHAFHFCISRMLKTRQVCPDNRREWEFOKYG 108
DB 61 ASATSECTVAMGVGNHAFHFCISRMLKTRQVCPDNRREWEFOKYG 108
RESULT 7
ABB68080
ID ABB68080 standard; protein, 108 AA.
XX
XX ABB68080;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 31032.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX
XX 11-JUL-2000; 2000US-0064150.

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XX (PEXE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li FWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX N-PSDB; ABL12183.
XX
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions.
XX
XX Disclosure; SEQ ID NO 31032; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
XX sequences (AB101840-AB16175) and the encoded proteins (AB57737-
XX AB872072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 108 AA:
SQ
Query Match 86.7%; Score 534; DB 4; Length 108;
Best Local Similarity 87.2%; Pred. No. 1.2e-54;
Matches 95; Conservative 4; Mismatches 4; Indels 6; Gaps 2;
QY 5 MDVD-----TSGTNSGSGKGRFEYKKNVAVLWMDIVNCAICRNHMDLCIECOAN 59
DB 1 MEVDEDGYEVPSSSKG-DKRFVEYKKNVAVLWMDIVNCAICRNHMDLCIECOAN 59
QY 60 QASATSECTVAMGVGNHAFHFCISRMLKTRQVCPDNRREWEFOKYG 108
DB 60 QASATSECTVAMGVGNHAFHFCISRMLKTRQVCPDNRREWEFOKYG 108
RESULT 8
AAG23004
ID AAG23004 standard; protein, 118 AA.
XX
XX AAG23004;
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 26148.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX
XX 05-MAR-1999; 99US-0123180P.
XX
XX 09-MAR-1999; 99US-0123548P.
XX
XX 23-MAR-1999; 99US-0125788P.
XX
XX 25-MAR-1999; 99US-0126264P.
XX
XX 29-MAR-1999; 99US-0126785P.
XX
XX 01-APR-1999; 99US-0127462P.
XX
XX 06-APR-1999; 99US-0128234P.
XX
XX 08-APR-1999; 99US-0128714P.
XX
XX 16-APR-1999; 99US-0129845P.
XX
XX 19-APR-1999; 99US-0130077P.

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PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134258P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136783P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139112P.
PR 16-JUN-1999; 99US-0139453P.
PR 16-JUN-1999; 99US-0139455P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
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PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142820P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.

PR 20-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144684P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
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PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 03-AUG-1999; 99US-0146389P.
PR 04-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 05-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147316P.
PR 09-AUG-1999; 99US-0147935P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
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PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
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PR 22-AUG-1999; 99US-0149930P.
PR 23-AUG-1999; 99US-0150566P.
PR 25-AUG-1999; 99US-0150884P.
PR 26-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151388P.
PR 01-SEP-1999; 99US-0151930P.
PR 01-SEP-1999; 99US-0152633P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
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PR 05-OCT-1999; 99US-0157533P.
PR 06-OCT-1999; 99US-0157855P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158212P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159299P.
PR 14-OCT-1999; 99US-0159330P.

PR	21-JUL-1999	99JUS-0144811P
PR	21-JUL-1999	99JUS-0140086P
PR	21-JUL-1999	99JUS-0145088P
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PR	27-JUL-1999	99JUS-0145918P
PR	27-JUL-1999	99JUS-0145919P
PR	28-JUL-1999	99JUS-0145951L
PR	02-AUG-1999	99JUS-0146386P
PR	02-AUG-1999	99JUS-0146388P
PR	02-AUG-1999	99JUS-0146389P
PR	03-AUG-1999	99JUS-0147038P
PR	04-AUG-1999	99JUS-0147204P
PR	05-AUG-1999	99JUS-0147302P
PR	05-AUG-1999	99JUS-0147392P
PR	05-AUG-1999	99JUS-0147260P
PR	06-AUG-1999	99JUS-0147303P
PR	06-AUG-1999	99JUS-0147416P
PR	09-AUG-1999	99JUS-0147935P
PR	09-AUG-1999	99JUS-0147935P
PR	10-AUG-1999	99JUS-0148171P
PR	11-AUG-1999	99JUS-0148319P
PR	12-AUG-1999	99JUS-0148341P
PR	13-AUG-1999	99JUS-0148565P
PR	13-AUG-1999	99JUS-0148684P
PR	16-AUG-1999	99JUS-0149368P
PR	17-AUG-1999	99JUS-0149175P
PR	18-AUG-1999	99JUS-0149426P
PR	20-AUG-1999	99JUS-0149722P
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PR	23-AUG-1999	99JUS-0149902P
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PR	25-AUG-1999	99JUS-0149930P
PR	26-AUG-1999	99JUS-0150566P
PR	27-AUG-1999	99JUS-0150884P
PR	27-AUG-1999	99JUS-0151065P
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PR	30-AUG-1999	99JUS-0151303P
PR	31-AUG-1999	99JUS-015138P
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PR	23-SEP-1999	99JUS-0155589P
PR	28-SEP-1999	99JUS-0156458P
PR	29-SEP-1999	99JUS-0156569P
PR	04-OCT-1999	99JUS-0157117P
PR	05-OCT-1999	99JUS-0157753P
PR	06-OCT-1999	99JUS-0157865P
PR	07-OCT-1999	99JUS-0158029P
PR	08-OCT-1999	99JUS-0158323P
PR	12-OCT-1999	99JUS-0158363P
PR	12-OCT-1999	99JUS-0158396P
PR	13-OCT-1999	99JUS-0159294P
PR	13-OCT-1999	99JUS-0159295P
PR	14-OCT-1999	99JUS-0159329P
PR	14-OCT-1999	99JUS-0159330P
PR	14-OCT-1999	99JUS-0159337P
PR	14-OCT-1999	99JUS-0159637P
PR	14-OCT-1999	99JUS-0159638P

PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160890P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161930P.
PR 28-OCT-1999; 99US-0161932P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match	83.0%	Score 511; DB 3;	Length 109;
Best Local Similarity	88.8%	Pred. No. 6	3e-52;
Matches 87; Conservative	5;	Mismatches 6;	Indels 0; Gaps 0;

QY 1 SGTSGAGKRFEEYKKNNVALVAMDIVDNCACRHHIMDLCEQCANQASATSECTV 70
:::
Db 12 AASSNNKAKRFEIKKMSAVALVAMDIVDNCACRHHIMDLCEQCANQASATSECTV 71

QY 71 AMGVCAAFHHCISRLKTRQVCPDNNREMEPKYGH 108
|||||
Db 72 AMGVCAAFHHCISRLKTRQVCPDNNSEMEPKYGH 109

```

RESULT 10
AB86109
ID   AB86109 standard; protein, 122 AA.
XX
XX   AB86109;
AC
DE   Drosophila melanogaster polypeptide SEQ ID NO 25119.
XX
XX   Drosophila/developmental biology/ cell signalling; insecticide;
XX   pharmaceutical.
XX
XX   Drosophila melanogaster.
OS
XX   WO200171042-A2.
XX
XX   27-SEP-2001.
PN
PD
PF   23-MAR-2001; 2001WO-US009231.
XX
XX   23-MAR-2000; 2000US-0191637P.
PR   11-JUL-2000; 2000US-00614150.
XX
XX   (PEKE ) PE CORP NY.
PA
XX   Venter JC, Adams M, Li PWD, Myers EW;
XX   WPI; 2001-656860/75.
XX   N-PDB; ABL10212.
DR
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions.
XX
PS   Disclosure; SEQ ID NO 25119; 21pp + sequence listing; English.
XX
XX   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is

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CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pot_sequences
 XX

SO Sequence 122 AA;

Query Match 65.0%; Score 400.5; DB 4; Length 122;
 Best Local Similarity 65.4%; Pred. No. 6.7e-39;
 Matches 70; Conservative 13; Mismatches 19; Indels 5; Gaps 2;

OY 5 MDVDTPEGTNSG-AGKKEFEKKNNAVAMWDIVDNCACRHHIMDLCECOANO 60
 DB 16 MDNDDEPSSGSGAVQARTERFVKKVMVAHAMGMVAVDNCAICRHHIMDLCECOAD- 74
 OY 61 ASATSECTVAMGVGNHAFHFHCISRWLKTRQVCPLDNRMEFQKYG 107
 DB 75 PNNODECTVAMGECNHAFFHCIAFWLKTRLCPLDNRMEWYQKYG 121

RESULT 11

AB08814 standard; protein; 121 AA.

AC AAB08814;

DT 02-JAN-2001 (first entry)

DE A yeast cullin-interacting RING-H2 finger protein (Rbx1).

XX Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;
 XX tumour suppressor; carcinoma; Ring box associated carcinoma;
 XX von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;
 XX cerebellar hemangioblastoma; hemangioma; retinal angiomatosis;
 XX pheochromocytomas.

OS Saccharomyces cerevisiae.

PN W0200050445-A1.

PD 31-AUG-2000.

PF 25-FEB-2000; 2000MO-US004838.

PR 26-FEB-1999; 99US-0121787P.

XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.

PA Conaway JA, Conaway RC, Kamura T;

XX WPI; 2000-572067/53.

DR N-PSDB; AAA74979.

PT Cullin interacting RING-H2 finger protein, a component of von Hippel-
 PT Lindau tumor suppressor complex and Skp1-Cdc53P-F-box protein (SCF)
 PT ubiquitin ligase, useful for diagnosing and treating Ring box protein
 PT associated carcinomas.

PS Disclosure, Page 34-35; 37pp; English.

XX The present sequence represents a yeast cullin-interacting RING-H2 finger
 CC protein (Ring box protein), designated Rbx1. The human Rbx1 polypeptide
 CC is a tumour suppressor. Human Rbx1 is useful for diagnosing a
 CC predisposition of a patient to certain carcinomas. It is also useful for
 CC treating Ring box protein associated carcinomas or augmenting
 CC metabolically deficient systems in animals. Human Rbx1 is also useful for
 CC evaluating the effectiveness of a therapeutic treatment for Ring box
 CC associated carcinomas. Human Rbx1 can be used to screen for agents which
 CC augment or inhibit the activity of other cullin-containing ubiquitin

CC ligase and of the VHL (von Hippel-Lindau) complex controlling the
 CC conjugation of ubiquitin or ubiquitin-like proteins to various sets of
 CC target proteins. Carcinomas which may be treated include renal
 CC carcinomas, cerebellar hemangioblastomas and hemangiomas, retinal
 CC angiomatosis and pheochromocytomas
 XX

SO Sequence 121 AA;

Query Match 62.5%; Score 385; DB 3; Length 121;
 Best Local Similarity 56.6%; Pred. No. 4.4e-37;
 Matches 64; Conservative 10; Mismatches 29; Indels 10; Gaps 1;

OY 5 MDVDTPEGTNSGAG-----KKRFEYKKNNAVAMWDIVDNCACRHHIMDLCE 54
 DB 8 MDVDEDSQNIAGSSNOSAFVETKRFELKKMTAVAFMSWDIAVDNCAICRHHIMDLCE 67
 OY 55 EQQANQASATSECTVAMGVGNHAFHFHCISRWLKTRQVCPLDNRMEFQKYG 107
 DB 68 ECPKAMTDIDNECVAMGVGNHAFHFHCISRWLKTRQVCPLDNRMEFQKYG 120

RESULT 12

AB041007 standard; protein; 57 AA.

AC AAB41007;

DT 08-FEB-2001 (first entry)

DE Human ORFX ORF771 polypeptide sequence SEQ ID NO:1542.

XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 XX vulnery; antiproliferative; antiparkinsonian; neurotrophic; neuroprotective;
 XX immunomodulant; osteoporotic; antiarthritic; immunosuppressant; cardiant;
 XX immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 XX hypotensive; dermatological; immunosuppressive; antineoplastic;
 XX antiviral; antibacterial; antifungal; antineumatic; antitumor;
 XX antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 XX neurodegenerative disorder; osteoarthritis; graft vs host disease;
 XX cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 XX cholesterol ester storage; systemic lupus erythematosus; infection;
 XX severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 XX allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 XX bone damage; cartilage damage; antineoplastic disease; coagulation;
 XX thrombosis; contraceptive.

OS Homo sapiens.

PN W0200058473-A2.

PD 05-OCT-2000.

PF 31-MAR-2000; 2000MO-US008621.

PR 31-MAR-1999; 99US-0127607P.

PR 02-APR-1999; 99US-0127636P.

PR 05-APR-1999; 99US-0127728P.

PR 30-MAR-2000; 2000US-00540763.

PA (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2000-602362/57.

DR N-PSDB; AAC75216.

PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease.

PS Claim 11; Page 1266; 5507pp; English.
 XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC

CC which represent the human ORF open reading frames 1 to 3161. The ORF
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
 CC antiproliferative; antiparkinsonian; neurotrophic; neuroprotective; osteopathic;
 CC anticonvulsant; antidiabetic; immunosuppressant; immunostimulant;
 CC cardiact; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
 CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
 CC antiviral; antifungal; antihemetic; antihypertensive; antidiabetic. The
 CC sequences can be used for determining the presence of or predisposition
 CC to, or preventing or treating pathological conditions associated with an
 CC ORF-associated disorder. The nucleic acids can be used to express ORF
 CC proteins in gene therapy vectors. The proteins and nucleic acids may be
 CC used to treat cancers, proliferative disorders, neurodegenerative
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
 CC storage, systemic lupus erythematosus, severe combined immunodeficiency
 CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
 CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
 CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive

SO Sequence 57 AA:

Query Match 52.4%; Score 323; DB 3; Length 57;
 Best Local Similarity 100.0%; Pred. No. 3.4e-30;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

54 IECQANQASATSEECTVANGVGNHAFHFCISRWLKTQVCPDLNREWEFOCKYGH 108
 Db 3 IECQANQASATSEECTVANGVGNHAFHFCISRWLKTQVCPDLNREWEFOCKYGH 57

RESULT 13
 AAY06492
 ID AAY06492 standard; protein: 113 AA.
 XX
 AC AAY06492;
 XX
 DT 27-SEP-1999 (first entry)
 XX
 DE Human sensitive to apoptosis (SAG) protein.
 XX
 KM SAG protein; sensitive to apoptosis; human; cancer; tumour;
 KM neurodegenerative disease; muscular dystrophy; wound healing; vulnary;
 KM therapy.
 XX
 OS Homo sapiens.
 XX
 XX
 XX Key Location/Qualifiers
 XX FH 16..27
 XX FT /note= "prokaryotic membrane lipoprotein lipid attachment
 XX FT site"
 XX FT 47..51
 XX FT /note= "haem binding site"
 XX FT 49..66
 XX FT /note= "somatotropin, prolactin and related hormone
 XX FT motif"
 XX FT 50..54
 XX FT /note= "haem binding protein"
 XX FT 54..63
 XX FT /note= "aminoacyl-tRNA class II motif"
 XX FT 65..107
 XX FT /note= "Ly-6/U-par domain"
 XX FT 85..107
 XX FT /note= "Kazal serine protease inhibitor motif"
 XX PN
 XX MO9932514-A2.
 XX
 XX 01-JUL-1999.
 XX
 XX 15-DEC-1998; 98MO-US026705.
 XX PF
 XX 19-DEC-1997; 97US-0068179P.
 XX PR
 XX 11-SEP-1998; 98US-0099840P.
 PD

XX (WARN) WARNER LAMBERT CO.
 PA
 XX
 XX Sun Y;
 XX
 XX WPI; 1999-430152/56.
 DR N-PSDB; AAX87314.
 XX
 XX SAG: Sensitive to Apoptosis Gene and related proteins, useful for
 PT promoting cell growth and protecting cells against apoptosis.
 FT
 XX
 XX Claim 20; Page 51-52; 84pp; English.
 PS
 XX
 XX This sequence represents a novel human redox-sensitive, haem-binding
 CC protein with a zinc RING finger domain that is encoded by the SAG gene
 CC (see AAX87314). SAG promotes cell growth, protects cells from apoptosis,
 CC scavenges oxygen radicals and can be used for the reversion of a tumour
 CC phenotype. SAG is highly conserved among species. Disruption in Yeast was
 CC shown to be lethal. SAG deletion mutants (see AAX87315-16) have been
 CC identified in human cancer lines, suggesting a role in carcinogenesis.
 CC SAG genes, and mutant SAG genes, can be used to protect cells from
 CC apoptosis induced by redox reagents. Antisense SAG genes can be used to
 CC inhibit the growth of tumour cells. The SAG genes can also be used for
 CC the recombinant production of the SAG proteins. The SAG proteins can be
 CC used to scavenge oxygen radicals in organisms and to promote wound
 CC healing. They are also ideal molecular targets in the development of
 CC drugs against neurodegenerative disorders, cancers and muscle dystrophy

SO Sequence 113 AA:

Query Match 47.4%; Score 292; DB 2; Length 113;
 Best Local Similarity 50.5%; Pred. No. 3.3e-26;
 Matches 49; Conservative 14; Mismatches 30; Indels 4; Gaps 2;

11 SGTNSGAKGRFEYKKNVAVLWMDIYVNCNACISRNHINDLIECQANQASATSECTV 70
 Db 20 SGRKSG-GDKMFSIKKNVAVLWMDIYVNCNACISRNHINDLIECQANQASATSECTV 75

71 AMGVGNHAFHFCISRWLKTQVCPDLNREWEFOCKYGH 107
 QY 76 VMGECNHSFHCNCSLWVKNRCPDLCQDDVVQIRIG 112
 Db

RESULT 14
 AAB43295
 ID AAB43295 standard; protein: 113 AA.
 XX
 XX AAB43295;
 XX
 XX 08-FEB-2001 (first entry)
 XX
 DE Human ORF3059 polypeptide sequence SEQ ID NO:6118.
 XX
 XX
 XX Human; open reading frame; ORF; detection; cytostatic; hepatotropic;
 KM vulnary; antiproliferative; antiparkinsonian; neurotrophic; neuroprotective;
 KM anticonvulsant; osteopathic; antidiabetic; immunosuppressant; cardiact;
 KM immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KM hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KM antiviral; antibacterial; antifungal; antihemetic; antihypertensive;
 KM antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
 KM neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KM cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KM cholesterol ester storage; systemic lupus erythematosus; infection;
 KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KM bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KM thrombosis; contraceptive.
 XX
 XX Homo sapiens.
 XX
 XX
 XX WO200058473-A2.
 XX PN
 XX 05-OCT-2000.
 PD

XX 31-MAR-2000; 2000WO-US008621.
 PF 31-MAR-1999; 99US-0127607P.
 PR 02-APR-1999; 99US-0127666P.
 PR 05-APR-1999; 99US-0127288P.
 PR 30-MAR-2000; 2000US-00540763.
 XX (CURA-) CURAGEN CORP.
 XX Shinkets RA, Leach M;
 DR WPI, 2000-602362/57.
 DR N-PSDB; AAC77504.
 XX Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease.
 PS Claim 11; Page 5300-5301; 5507pp; English.
 XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORF open reading frames 1 to 3161. The ORF
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
 CC antiproliferative; antiparasitic; neuroprotective; osteopathic;
 CC anticonvulsant; antihypertensive; immunosuppressant; immunostimulant;
 CC cardiatic; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
 CC dermatologic; immunosuppressive; antineoplastic; antibacterial;
 CC antiviral; antifungal; antihelminthic; antiparasitic. The
 CC sequences can be used for determining the presence of or predisposition
 CC to, or preventing or treating pathological conditions associated with an
 CC ORF-associated disorder. The nucleic acids can be used to express ORF
 CC proteins in gene therapy vectors. The proteins and nucleic acids may be
 CC used to treat cancers, proliferative disorders, neurodegenerative
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
 CC storage, systemic lupus erythematosus, severe combined immunodeficiency
 CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
 CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
 CC cartilage damage, nocturnal haemoglobinuria, anti-inflammatory disease; to
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
 XX SQ Sequence 113 AA;
 Query Match 47.4%; Score 292; DB 3; Length 113;
 Best Local Similarity 50.5%; Pred. No. 3.3e-26;
 Matches 49; Conservative 14; Mismatches 30; Indels 4; Gaps 2;
 QY 11 SGTNGAGKRFVKKNNVALLMWDIVDNCALCRHIMDLCTECOMNQSATSECTV 70
 DB 20 SSSKSG-GDKMPSLKKNNVAVMWSVDECDTALCRVWDACLRQEN---KQEDCV 75
 QY 71 AMGVCHAHFHFCISRLKTRQVCPIDNREWEFOYCY 107
 DB 76 VMGECHSHFHCNCSLWVKNNRCPLCQDDWVQIG 112
 RESULT 15
 AAU15873
 ID AAU15873 standard; protein; 118 AA.
 XX AAU15873;
 XX 07-NOV-2001 (first entry)
 DE Human novel secreted protein, Seq ID 826.
 XX Human; immunosuppressive; antihypertensive; antineoplastic; cytostatic;
 KW cardiatic; vasotropic; cerebroprotective; neurotropic; neuroprotective;
 KW antibacterial; vitucide; fungicide; opthalmological; vulnary;
 KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
 KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
 KW cerebral ischaemia; angiogenesis; nervous system disorder;

KW Alzheimer's disease; infection; ocular disorder; corneal infection;
 KW wound healing; epithelial cell proliferation; skin ageing; food additive;
 KW preservative; antiproliferative.
 OS Homo sapiens.
 PN MO200155322-A2.
 XX 02-AUG-2001.
 XX 17-JAN-2001; 2001WO-US001341.
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-021680P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220964P.
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 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
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 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
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 PR 22-AUG-2000; 2000US-0226681P.
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 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 12-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 25, 2004, 09:33:42 ; Search time 22 Seconds
(without alignments)
253.437 Million cell updates/sec

Title: US-09-914-324a-1

Sequence: 1 MAAMADVDPSTGNSAGKK.....KTRQVCPDNRWEFOYGH 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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5: /cgn2_6/prodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfltest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	208	33.8	84	US-09-599-360B-77	Sequence 77, Appl
2	185	30.0	112	US-09-621-976-5677	Sequence 5677, Ap
3	185	30.0	112	US-09-621-976-5805	Sequence 5805, Ap
4	105.5	17.1	94	US-09-621-976-5714	Sequence 5714, Ap
5	85	13.8	664	US-09-268-140-2	Sequence 2, Appl
6	83	13.5	104	US-09-325-932A-49	Sequence 49, Appl
7	83	13.5	337	US-09-828-303-18	Sequence 18, Appl
8	80	13.0	180	US-08-786-606-3	Sequence 3, Appl
9	80	13.0	180	US-08-933-750C-48	Sequence 48, Appl
10	80	13.0	180	US-09-234-613-48	Sequence 48, Appl
11	80	13.0	284	US-08-786-606-9	Sequence 9, Appl
12	79	12.8	50	US-09-052-089A-15	Sequence 15, Appl
13	79	12.8	359	US-09-663-600A-106	Sequence 106, App
14	79	12.8	381	US-08-867-057-1	Sequence 1, Appl
15	79	12.8	381	US-08-867-057-3	Sequence 3, Appl
16	79	12.8	381	US-09-128-369-1	Sequence 1, Appl
17	79	12.8	381	US-09-128-369-3	Sequence 3, Appl
18	79	12.8	381	US-09-128-369-3	Sequence 3, Appl
19	79	12.8	410	US-09-663-600A-700	Sequence 200, App
20	76.5	12.4	317	US-07-945-283-4	Sequence 4, Appl
21	76.5	12.4	1302	US-09-921-099A-8	Sequence 8, Appl
22	76	12.3	4	US-09-423-890-2	Sequence 2, Appl
23	76	12.3	1593	US-08-628-828-8	Sequence 8, Appl
24	76	12.3	305	US-08-628-828-9	Sequence 114, App
25	74.5	12.1	67	US-07-945-283-5	Sequence 5, Appl
26	74.5	12.1	149	US-09-690-454-205	Sequence 205, App
27	74.5	12.1	166	US-09-690-454-204	Sequence 204, App

28	74.5	12.1	826	US-09-894-998A-47	Sequence 47, Appl
29	73	11.9	551	US-08-699-103B-25	Sequence 25, Appl
30	73	11.9	551	US-09-229-059-25	Sequence 25, Appl
31	73	11.9	551	US-09-628-133-25	Sequence 25, Appl
32	72.5	11.8	66	US-09-205-258-1030	Sequence 1030, Ap
33	72.5	11.8	69	US-07-945-283-6	Sequence 6, Appl
34	72.5	11.8	84	US-09-205-258-1032	Sequence 1032, Ap
35	72.5	11.8	167	US-09-205-258-1026	Sequence 1026, Ap
36	72.5	11.8	276	US-08-786-606-5	Sequence 5, Appl
37	72.5	11.8	276	US-09-205-258-1027	Sequence 1027, Ap
38	72.5	11.8	341	US-09-205-258-1034	Sequence 1034, Ap
39	71	11.5	40	US-09-046-894-44	Sequence 44, Appl
40	71	11.5	199	US-09-325-932A-46	Sequence 46, Appl
41	70.5	11.4	46	US-08-691-814B-17	Sequence 17, Appl
42	67.5	11.0	49	US-09-230-637-60	Sequence 60, Appl
43	67	10.9	395	US-08-841-349-9	Sequence 9, Appl
44	67	10.9	395	US-09-431-184A-9	Sequence 9, Appl
45	66	10.7	67	US-07-945-283-7	Sequence 7, Appl

ALIGNMENTS

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RESULT 1
US-09-599-360B-77
Sequence 77, Application US/09599360B
Patent No. 6548633
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Bouguetere, L.
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: GENSET, 0500C93
CURRENT APPLICATION NUMBER: US/09/599,360B
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/469,099
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patent.pm
SEQ ID NO 77
LENGTH: 84
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-599-360B-77
Query Match
Best Local Similarity 37.5% Score 208; DB 4; Length 84;
Matches 33; Conservative 17; Mismatches 30; Indels 8; Gaps 2;
QY 21 RFEVKMNAVALMAMDIWDNCALGRNIMDLCTECQANASATSECTYAMGVCHNATH 80
DB 2 KYKIKCMNGVATWLMVANDERCGICRMAFNGCCPDCK---VPGDDCLPLWQCSCHPH 56
QY 81 FHCISRMLKTRQV---CPDNRWEFOY 105
DB 57 MHCITKMLHAQVQCHRCMCRGWEKPE 84
RESULT 2
US-09-621-976-5677
Sequence 5677, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET, 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
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;; CURRENT FILING DATE: 2000-07-21
;; NUMBER OF SEQ ID NOS: 19335
;; SOFTWARE: Patent.pm
;; SEQ ID NO 5677
;; LENGTH: 112
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: -106...-1
US-09-621-976-5677

Query Match 30.0%; Score 185; DB 4; Length 112;
Best Local Similarity 38.0%; Pred. No. 5.1e-13;
Matches 30; Conservative 13; Mismatches 28; Indels 8; Gaps 2;

QY 21 REEVKKNVAVLAWMDIVVNCALICRNHIMDLCECQANQASATSECTVAMGVCHAFH 80
DB 2 KYKIKCMNGVATWLVANDENCGICRMAFNGCCPDCK-----VGDGDCPLVMGQCSCHFH 56
QY 81 FHCISRMLKTRGV---CPL 96
DB 57 MHCILKMLHAQVQCHCPM 75

RESULT 3
US-09-621-976-5805
;; Sequence 5805, Application US/09621976
;; Patent No. 6639063
;; GENERAL INFORMATION:
;; APPLICANT: Dumas Milne Edwards, J.B.
;; APPLICANT: Jodert, S.
;; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;; FILE REFERENCE: GENSET.054PR2
;; CURRENT APPLICATION NUMBER: US/09/621,976
;; CURRENT FILING DATE: 2000-07-21
;; NUMBER OF SEQ ID NOS: 19335
;; SOFTWARE: Patent.pm
;; SEQ ID NO 5805
;; LENGTH: 112
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: -109...-1
US-09-621-976-5805

Query Match 30.0%; Score 185; DB 4; Length 112;
Best Local Similarity 38.0%; Pred. No. 5.1e-13;
Matches 30; Conservative 13; Mismatches 28; Indels 8; Gaps 2;

QY 21 REEVKKNVAVLAWMDIVVNCALICRNHIMDLCECQANQASATSECTVAMGVCHAFH 80
DB 2 KYKIKCMNGVATWLVANDENCGICRMAFNGCCPDCK-----VGDGDCPLVMGQCSCHFH 56
QY 81 FHCISRMLKTRGV---CPL 96
DB 57 MHCILKMLHAQVQCHCPM 75

RESULT 4
US-09-621-976-5714
;; Sequence 5714, Application US/09621976
;; Patent No. 6639063
;; GENERAL INFORMATION:
;; APPLICANT: Dumas Milne Edwards, J.B.
;; APPLICANT: Jodert, S.
;; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;; FILE REFERENCE: GENSET.054PR2
;; CURRENT APPLICATION NUMBER: US/09/621,976
;; CURRENT FILING DATE: 2000-07-21

;; NUMBER OF SEQ ID NOS: 19335
;; SOFTWARE: Patent.pm
;; SEQ ID NO 5714
;; LENGTH: 94
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: -53...-1
;; NAME/KEY: UNSURE
;; LOCATION: 14
;; OTHER INFORMATION: Xaa = Glu, Gln
US-09-621-976-5714

Query Match 17.1%; Score 105.5; DB 4; Length 94;
Best Local Similarity 36.6%; Pred. No. 0.00022;
Matches 15; Conservative 8; Mismatches 13; Indels 5; Gaps 1;

QY 48 HIMDLCECQANQASATSECTVAMGVCHAFHFCISRML 88
DB 10 HLTDAAPDCK-----VGDGDCPLVMGQCSCHFHMLKML 45

RESULT 5
US-09-268-140-2
;; Sequence 2, Application US/09268140
;; Patent No. 6268176
;; GENERAL INFORMATION:
;; APPLICANT: Gemmill, Robert M.
;; APPLICANT: Drabkin, Harry A.
;; TITLE OF INVENTION: TRCS, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED
;; FILE REFERENCE: 93445-00004
;; CURRENT APPLICATION NUMBER: US/09/268,140
;; PRIOR FILING DATE: 2000-03-12
;; PRIOR APPLICATION NUMBER: US 60/077,723
;; PRIOR FILING DATE: 1998-03-12
;; NUMBER OF SEQ ID NOS: 46
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 664
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-268-140-2

Query Match 13.8%; Score 85; DB 3; Length 664;
Best Local Similarity 28.6%; Pred. No. 0.34; 22; Indels 28; Gaps 4;
Matches 24; Conservative 10; Mismatches 13; Indels 28; Gaps 4;

QY 20 REEVKKNVAVLAWMDI-----VVDNCAICRNHIMDLCECQANQASATSECTVAM 72
DB 522 RRTAVKRINSIP---EIKSRLQEIINDVCAICYHEF-----TTSARIT--- 561
QY 73 GVCNHAFFHCISRMLKTRGVCP 96
DB 562 -PCNHYFHALCKRMILYIDTCM 584

RESULT 6
US-09-325-932A-49
;; Sequence 49, Application US/09325932A
;; Patent No. 6451604
;; GENERAL INFORMATION:
;; APPLICANT: Flinn, Barry
;; APPLICANT: Lasham, Annette
;; TITLE OF INVENTION: Compositions affecting programmed cell
;; FILE REFERENCE: 1022
;; CURRENT APPLICATION NUMBER: US/09/325,932A
;; CURRENT FILING DATE: 1999-06-04
;; NUMBER OF SEQ ID NOS: 206
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 49
;; LENGTH: 104

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TYPE: PRT
ORGANISM: Pinus radiata
US-09-325-932A-49

Query Match 13.5%; Score 83; DB 4; Length 104;
Best Local Similarity 30.9%; Pred. No. 0.071;
Matches 17; Conservative 4; Mismatches 20; Indels 14; Gaps 1;

QY 42 CAICRNHMDLCEQANQASATSECTVAMGVCHAFHFCISRWLTKRQVCP 96
DB 25 CAVCLSKFEDI-----EILRLPKCHAFHIDCIDVWLEKHSKCP 65

RESULT 7
US-09-828-303-18
Sequence 18, Application US/09828303
Patent No. 6677504
GENERAL INFORMATION:
APPLICANT: COSTA E SILVA, OSWALDO DA
APPLICANT: BOHNER, HANS J.
APPLICANT: VAN THIELEN, NOCHA
APPLICANT: CHEN, RONGYING
TITLE OF INVENTION: TRANSCRIPTION FACTOR STRESS-RELATED PROTEINS AND
FILE REFERENCE: 16313-0030
CURRENT APPLICATION NUMBER: US/09/828,303
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 18
LENGTH: 337
TYPE: PRT
ORGANISM: Physcomitrella patens
US-09-828-303-18

Query Match 13.5%; Score 83; DB 4; Length 337;
Best Local Similarity 29.3%; Pred. No. 0.27;
Matches 17; Conservative 7; Mismatches 20; Indels 14; Gaps 2;

QY 39 VDNCAICRNHMDLCEQANQASATSECTVAMGVCHAFHFCISRWLTKRQVCP 96
DB 85 VFCACVCL-----EFLGKRTLPK-----CHSTFLDCIDWMLHSHSTCP 128

RESULT 8
US-08-786-606-3
Sequence 3, Application US/08786606
Patent No. 5861495
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Au-Young, Janice
APPLICANT: Coleman, Roger
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN ZINC-BINDING
NUMBER OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,606
FILING DATE:

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy R
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0173 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-786-606-3

Query Match 13.0%; Score 60; DB 2; Length 180;
Best Local Similarity 28.2%; Pred. No. 0.28;
Matches 29; Conservative 12; Mismatches 18; Indels 44; Gaps 7;

QY 1 MAAMDVD-TPSGTN--SGAKKFEVKKNAVALAMWDIVDNCAICRNHMDLCEC 56
DB 1 MAASEEDGCEGPRERNGAG-ATFE-----CNICLLE-32

QY 57 QANQASATSECTVAMGVCHAFHFCISRWLTKRQVCP 96
DB 33 -----TARENVVS--VGHLYCWPCLHQLWLETRPRQECVP 66

RESULT 9
US-08-933-750C-48
Sequence 48, Application US/08933750C
Patent No. 5932442
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Giegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 556
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TESTNOT07
CLONE: 3217567
US-08-933-750C-48

Query Match 13.0%; Score 80; DB 2; Length 180;
Best Local Similarity 28.2%; Pred. No. 0.28; 18; Indels 44; Gaps 7;
Matches 29; Conservative 12; Mismatches 18; Indels 44; Gaps 7;

QY 1 MAAAMDVD-TPSGTN---SGAGKRPVKKNAVALMAMDIVDNCALCRNHIMDLICBC 56
DB 1 MAAAEEDGGPBPNNRGGAG-ATPE-----CNICLE- 32
QY 57 QANQASATSECTVANGVCNHAFFHCISRWTKT---RQVCPL 96
DB 33 -----TAREAVVS--VCGHLYCWPCLHQLWLETRPREOCEPV 66

RESULT 10
US-09-234-613-48
Sequence 48, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TESTNOT07
CLONE: 3217567
US-09-234-613-48

Query Match 13.0%; Score 80; DB 3; Length 180;
Best Local Similarity 28.2%; Pred. No. 0.28; 18; Indels 44; Gaps 7;
Matches 29; Conservative 12; Mismatches 18; Indels 44; Gaps 7;

QY 1 MAAAMDVD-TPSGTN---SGAGKRPVKKNAVALMAMDIVDNCALCRNHIMDLICBC 56
DB 1 MAAAEEDGGPBPNNRGGAG-ATPE-----CNICLE- 32
QY 57 QANQASATSECTVANGVCNHAFFHCISRWTKT---RQVCPL 96
DB 33 -----TAREAVVS--VCGHLYCWPCLHQLWLETRPREOCEPV 66

RESULT 11
US-08-786-606-9
Sequence 9, Application US/08786606
Patent No. 5861495
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Au-Young, Janice
APPLICANT: Coleman, Roger
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL HUMAN ZINC-BINDING
PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,606
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0173 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 284 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 157535
US-08-786-606-9
Query Match 13.0%; Score 80; DB 2; Length 284;
Best Local Similarity 25.5%; Pred. No. 0.47; 29; Indels 32; Gaps 3;
Matches 24; Conservative 9; Mismatches 29; Indels 32; Gaps 3;

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Qy 3 AAMDVTPSGTSGAGKREVEKKNAVALMAMDIYVNCALCRHIMDLICICQANQAS 62
Db 104 AAKMIPKTO-----KFSDEK-----DLUSDCAIC-----1E 131
Qy 63 ATSECTVAMGVGNHAFHFCISRWLKTROVCP 96
Db 132 AKRPTDTRILPCHEPHKNCIDPWLIEHRTCP 165

RESULT 12

US-09-052-089A-15
Sequence 15, Application US/09052089A
Patent No. 6346605

GENERAL INFORMATION:

APPLICANT: Lee, Soo Y.

Choi, Yongswon

TITLE OF INVENTION: SIGNAL TRANSDUCER FOR THE TGF RECEPTOR SUPER
FAMILY, AND USES THEREOF

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSER: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

FLOOR

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentia Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/052,089A

FILING DATE: 31-Mar-1998

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-198 CIP 1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 50 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-052-089A-15

Query Match 12.8%; Score 79; DB 4; Length 50;

Best Local Similarity 29.3%; Pred. No. 0.085; 15; Indels 16; Gaps 3;

Matches 17; Conservative 10; Mismatches 15; Indels 16; Gaps 3;

Qy 40 DNCAICRNHIMDLICICQANQASATSECTVAMGVGNHAFHFCISRWL-KTROVCP 96
Db 2 DVCAICLDDEYED-----GDKRLIL-PCSHAYHCKCVDPMWLTKTCTCPV 44

RESULT 13

US-09-663-600A-106

Sequence 106, Application US/09663600A

Patent No. 6573068

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean-Baptiste

APPLICANT: Duclert, Aymeric

APPLICANT: Bouguetier, Lydie

TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS

FILE REFERENCE: 31.US3.CIP

CURRENT APPLICATION NUMBER: US/09/663,600A

CURRENT FILING DATE: 2000-09-15

PRIOR APPLICATION NUMBER: 09/191,997

PRIOR FILING DATE: 1998-11-13

PRIOR APPLICATION NUMBER: 60/066,677

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/069,957

PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/074,121

PRIOR FILING DATE: 1998-02-09

PRIOR APPLICATION NUMBER: 60/081,563

PRIOR FILING DATE: 1998-04-13

PRIOR APPLICATION NUMBER: 60/096,116

PRIOR FILING DATE: 1998-08-10

PRIOR APPLICATION NUMBER: 60/099,273

PRIOR FILING DATE: 1998-09-04

NUMBER OF SEQ ID NOS: 229

SOFTWARE: Patent.pm

SEQ ID NO 106

LENGTH: 359

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: SIGNAL

NAME/KEY: UNSURE

LOCATION: 20,64,65,130,156,282,288,289,294,296,300,302,310

OTHER INFORMATION: Xaa = any one of the twenty amino acids

US-09-663-600A-106

Query Match 12.8%; Score 79; DB 4; Length 359;

Best Local Similarity 29.3%; Pred. No. 0.78; 15; Indels 16; Gaps 3;

Matches 17; Conservative 10; Mismatches 15; Indels 16; Gaps 3;

Qy 40 DNCAICRNHIMDLICICQANQASATSECTVAMGVGNHAFHFCISRWL-KTROVCP 96
Db 238 DVCAICLDDEYED-----GDKRLIL-PCSHAYHCKCVDPMWLTKTCTCPV 280

RESULT 14

US-08-867-057-1

Sequence 1, Application US/08867057

Patent No. 5840535

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Lal, Preeti

TITLE OF INVENTION: NEW ZINC RING PROTEIN

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/867,057

FILING DATE: Filed Herewith

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0311 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BMRBNOT02
CLONE: 104119
US-08-867-057-1

Query Match 12.8%; Score 79; DB 2; Length 381;
Best Local Similarity 29.3%; Pred. No. 0.84;
Matches 17; Conservative 10; Mismatches 15; Indels 16; Gaps 3;

QY 40 DNCAICRHHIMDLCIEQANQASATSECTVAMGVCNHAFFHCISRWL-KTROVCPPL 96
Db 238 DVCAICIDEYED-----GDKLRIL--PSSHVHCKCVDPMILTKTKTCPPV 280

RESULT 15

US-08-867-057-3
Sequence 3, Application US/08867057
Patent No. 5840535
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Shah, Parvi
TITLE OF INVENTION: NEW ZINC RING PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Inocyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,057
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0311 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1321818
US-08-867-057-3

Query Match 12.8%; Score 79; DB 2; Length 381;
Best Local Similarity 29.3%; Pred. No. 0.84;
Matches 17; Conservative 10; Mismatches 15; Indels 16; Gaps 3;

QY 40 DNCAICRHHIMDLCIEQANQASATSECTVAMGVCNHAFFHCISRWL-KTROVCPPL 96

Db 238 DVCAICIDEYED-----GDKLRIL--PSSHVHCKCVDPMILTKTKTCPPV 280

Search completed: March 25, 2004, 09:37:17
Job time : 23 secs

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OM protein - protein search, using sw model

Run on: March 25, 2004, 09:31:32 ; Search time 39 Seconds
(without alignments)
873,743 Million cell updates/sec

Title: US-09-914-324A-1

Perfect score: 616

Sequence: 1 MAAMVDYTPSGTNSGAKGK.....KTRQVCPDNRWEPQKXGH 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phase: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	523.5	85.0	114	10	Q863S0
2	523	84.9	110	10	Q7Y042
3	378	61.4	107	5	Q77367
4	314.5	51.1	97	10	Q9FTN1
5	308	50.0	92	5	Q8SW76
6	284.5	46.2	113	5	Q9V607
7	266	43.2	112	5	P91404
8	210	34.1	84	10	Q940X6
9	198	32.0	85	5	Q9VLU5
10	197	32.1	84	10	Q8H306
11	151	24.5	135	5	Q8IC8
12	146.5	23.8	57	10	Q9W910
13	141	22.9	165	3	Q12157
14	136	22.1	99	10	Q9AVZ5
15	132.5	21.5	94	3	Q86ZL9
16	129.5	21.0			

17	116.5	18.9	2160	5	Q17709	Q17709 caenorhabdi
18	112.5	18.3	911	3	Q66TDS	Q66TDS neurospora
19	106.5	17.3	189	10	Q84J02	Q84J02 cryza sativ
20	106	17.2	445	12	Q8QK70	Q8QK70 ectocarpus
21	104	16.9	349	10	Q9UD66	Q9UD66 arabidopsis
22	104	16.9	693	5	Q81U17	Q81U17 clona inter
23	102.5	16.6	249	10	Q9CASS	Q9CASS arabidopsis
24	102	16.6	151	10	Q9FI95	Q9FI95 arabidopsis
25	102	16.6	210	10	Q9SD55	Q9SD55 arabidopsis
26	100	16.2	147	10	Q9LTV5	Q9LTV5 arabidopsis
27	100	16.2	650	10	Q84WJ3	Q84WJ3 arabidopsis
28	100	16.2	676	10	Q9M1S2	Q9M1S2 arabidopsis
29	99.5	16.2	207	5	Q7Y115	Q7Y115 cryptospori
30	98	15.9	147	10	Q84WJ1	Q84WJ1 cryza sativ
31	98	15.8	158	10	Q9SRM0	Q9SRM0 arabidopsis
32	97.5	15.8	272	10	Q9FHA1	Q9FHA1 arabidopsis
33	97	15.7	159	10	Q8LZY8	Q8LZY8 arabidopsis
34	97	15.7	295	10	Q8H740	Q8H740 medicago sa
35	97	15.7	327	10	Q9C711	Q9C711 arabidopsis
36	96	15.6	332	10	Q9LQM2	Q9LQM2 arabidopsis
37	95.5	15.5	233	10	Q9FSZ7	Q9FSZ7 cicor arret
38	95.5	15.5	291	10	Q9SR08	Q9SR08 arabidopsis
39	95.5	15.5	356	10	Q9SS58	Q9SS58 arabidopsis
40	95.5	15.5	383	10	Q7XLY9	Q7XLY9 cryza sativ
41	95.5	15.5	441	10	Q3J446	Q3J446 arabidopsis
42	95	15.4	227	10	Q8LJB8	Q8LJB8 cryza sativ
43	95	15.4	322	10	Q9SMQ0	Q9SMQ0 arabidopsis
44	95	15.4	336	12	Q9VVP5	Q9VVP5 melamoplus
45	95	15.4	362	10	Q9LFF4	Q9LFF4 arabidopsis

ALIGNMENTS

RESULT 1

Q863S0

PRELIMINARY;

PRT; 114 AA.

AC Q863S0;

01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Putative ring box-1 protein.

GN 4911.12

Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Eriactoidae; Oryzaceae; Oryza.

NCBI_TaxID=39947;

OX [1]

SEQUENCE FROM N.A.

RP STRAIN=cv. Nipponbare;

RC Park Y.-U., Koshino N., Ramakrishna W., Sanmiguell P., Shiof B.,

RA Ma J., Jiang Z., Kleinholz A., Bennett J.,

RT "Sequence characterization of orthologous regions in the barley and

RT rice genomes."

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF480496; AL87158.1; -

DR Gramene; Q863S0; -

DR InterPro; IPR001841; Znf_ring.

DR Pfam; PF00097; Zf-C3HC4; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PSS0089; ZF_RING_2; 1.

DR SEQUENCE 114 AA; 12754 MW; 568633E0D733D5C CRC64;

QY Query Match

Best Local Similarity 84.4%; Pred. No. 2.9e-55; Length 114;

Matches 92; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 MAAMVDYTPSGTNSGAKG-KREFVKKNVAVALWAMDIVDNCALCNHIMDLCTICQAN 59

DB 6 VAVAVPSSIGASSGAKGKRFRIKKNVSLWAMDIVDNCALCNHIMDLCTICQAN 65

QY 60 QASATSECTAVANGVCHAFHFHCISRWLKTROVCPDNRWEPQKXGH 108

Db 66 QASATSECTVAMGVCNHAHFHFCISRMLKTRQVCPLDSEWSEFQYGH 114

RESULT 2

Q7Y042 PRELIMINARY; PRT; 110 AA.
 AC Q7Y042;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Ring box protein.
 OS Populus tomentosa.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
 OC NCBI_TaxID=118781;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fan J.H.;
 RT "Ring-box protein (Pcrbx1) of Populus tomentosa."
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY02066; AAP57304.1; -
 SQ SEQUENCE 110 AA; 12591 MW; 0172C6CAE3FA2772 CRC64;

Query Match 84.9%; Score 523; DB 10; Length 110;
 Best Local Similarity 84.5%; Pred. No. 3.3e-55;
 Matches 93; Conservative 4; Mismatches 7; Indels 6; Gaps 2;

QY 5 MDVD---TPSG---TNSGAGKRPFEVKKNNVALMWDIVDNCALCRNHIMDLCEQA 58
 Db 1 MDIDVTWVPAGEASSSSSRKPKREIKKNAVALMWDIVDNCALCRNHIMDLCEQA 60

QY 59 NQASATSECTVAMGVCNHAHFHFCISRMLKTRQVCPLDSEWSEFQYGH 108
 Db 61 NQASATSECTVAMGVCNHAHFHFCISRMLKTRQVCPLDSEWSEFQYGH 110

RESULT 3

Q77367 PRELIMINARY; PRT; 107 AA.

AC Q77367;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Putative ring finger protein.

GN MAJ3P6.28. falciparum (isolate 3D7).
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OC NCBI_TaxID=36329;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=3D7;

RA MEDLIN=99376085; PubMed=10448855;
 RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
 RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
 RA Gentles S., Gilliam R., Hamlin N., Harris D., Holtroyd S., Hornsby T.,
 RA Horrocks P., Jagsal K., Jagsal B., Kyes S., McLean U., Moulé S.,
 RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
 RA Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
 RA Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
 RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
 falciparum."
 RL Nature 400:532-538 (1999).
 DR EMBL: Z98551; CAB1123.3; -
 DR PIR: T18513; T18513.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4_1.
 DR SMART: SM00184; RING_1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 SQ SEQUENCE 107 AA; 12419 MW; C563432A60F20262 CRC64;

Query Match 61.4%; Score 378; DB 5; Length 107;

Best Local Similarity 69.6%; Pred. No. 9.3e-38;
 Matches 64; Conservative 5; Mismatches 15; Indels 8; Gaps 1;

QY 22 FEVKKNNVALMWDIVDNCALCRNHIMDLCEQA-----NQASATSECTVAMG 73

Db 13 FKHKMSAVAAWSDIVDNCALCRNHIMDLCEQAKTTHDNDXKIDKSGCTVAMG 72

QY 74 VCNHAFHFCISRMLKTRQVCPLDSEWSEFQY 105

Db 73 VCNHAFHFCISRMLKTRQVCPLDSEWSEFQY 104

RESULT 4

Q9FTN1 PRELIMINARY; PRT; 97 AA.
 AC Q9FTN1;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE P0005A05.18 protein (P0482C06.1 protein).
 GN P0005A05.18 OR P0482C06.1.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsunoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 clone: P0005A05."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

QY 12
 Db 12
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsunoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 clone: P0482C06."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AP002863; BAB16914.1; -
 DR EMBL: AP002845; BAB78605.1; -
 DR Gramene: Q9FTN1; -
 SQ SEQUENCE 97 AA; 10329 MW; F6DD1CE7BEDBA579 CRC64;

Query Match 51.1%; Score 314.5; DB 10; Length 97;
 Best Local Similarity 69.4%; Pred. No. 3.8e-30;
 Matches 59; Conservative 5; Mismatches 4; Indels 17; Gaps 2;

QY 6 DVDTP-----SGTNSGAG-----KKRFEVKKNNVALMWDIVDNCALCRNH 48

Db 4 DINAPPPAPAPAGAGGSSSAAGSSSRKPKREIKKNNVALMWDIVDNCALCRNH 63

QY 49 IMDLCIEQANQASATSECTVAMG 73

Db 64 IMDLCIEQANQASATSECTVAMG 88

RESULT 5

Q8SWU6 PRELIMINARY; PRT; 92 AA.

AC Q8SWU6;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein EC001_1095.

GN EC001_1095.
 OS Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.

OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.

OC NCBI_TaxID=6035;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=GB-M1;

RA Genoscope;
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RC SEQUENCE FROM N.A.
 RP STRAIN=GB-M1;
 RX MEDLINE=21576510; PubMed=11719806;
 RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
 RA Premier G., Barde V., Peyretallade E., Brottier P., Winkler P.,
 RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
 RA Weissenbach J., Vivas C.F.;
 RT "Genome sequence and gene compaction of the eukaryote parasite
 RT "Encephalitozoon cuniculi.";
 RL Nature 414:450-453(2001).
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AJ391737; CDD24981.1; -;
 DR InterPro: IPR001841; Znf_fing.
 DR Pfam: PF00097; Zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KM Hypochemical protein; Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 92 AA; 10807 MW; 2B04FEEAF093084 CRC64;

Query Match 50.0%; Score 308; DB 5; Length 92;
 Best Local Similarity 56.5%; Pied. No. 2,2e-29;
 Matches 48; Conservative 16; Mismatches 19; Indels 2; Gaps 1;

QY 19 KKRFEVKNNVAVLWMDIVDNCALCRNHNMDLCIECOANQASATSECTVANGVCNHA 78
 Db 4 KEIKLKAKNNVAVLWMDIVDNCALCRNHNMDLCIECOANQASATSECTVANGVCNHA 61

QY 79 FFFHCISRMVKTRQVCPDLDNREMEF 103
 Db 62 FFFHCISRMVKTRQVCPDLDNREMEF 86

RESULT 6
 QY9607 PRELIMINARY; PRT; 113 AA.
 AC QY9607;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE CG8998 protein (R61847p).
 OS CG8998.
 GN Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortran J.R., Yandell M.D., Zhang C., Chen L.X.,
 RA Brandon R.C., Rogers J.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burris J.M., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fiesler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegian C.,
 RA Jaitli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang X., Lin X.,
 RA Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshfegh A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Morley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 [2]
 RP SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Barzon J.J., An H., Baldwin D., Barzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Fafan D.,
 RA Ferrler S., Frise E., Galie R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibsgen C., Jaitli M., Kruse D., Li P., Mattei B., Moshfegh A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacle J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of Drosophila melanogaster genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman D., Carlson J.W., Celniker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of Drosophila melanogaster genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortran J.R., Yandell M.D., Zhang C., Chen L.X.,
 RA Brandon R.C., Rogers J.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burris J.M., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fiesler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegian C.,
 RA Jaitli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Query Match 46.2%; Score 284.5; DB 5; Length 113;

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Best Local Similarity 46.2%; Pred. No. 1,3e-26;
Matches 48; Conservative 18; Mismatches 35; Indels 3; Gaps 2;

QY 7 VDPSPGT-NSGAGKREVEKNNVAVLWMDIVDNCALCRNHIMDLCECQANQASAC- 64
DB 9 VDEPTDGDGAKREKMTLTKNNVAVMSWDECDICALCRVQVMSCLRCQADNDRDW 68
QY 65 -SEECTVAVGVCVCHAFHFCISRMKTRQVCPDNNREWEFOXKG 107
DB 69 GRQDCVAVWGECNHSFHHCCMSLWVKQNNRCPLQCEQWSTIQRMG 112

RESULT 7

ID P91404 PRELIMINARY; PRT; 112 AA.
AC P91404;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE R10A10.2 protein.
GN R10A10.2
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditicoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RX MEDLINE=94150118; PubMed=7906398;
RA Wilson R., Ahnscough R., Anderson K., Baynes C., Berts M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fillion L.,
RA Craxton M., Dear S., Di Z., Durbin R., Faveilo A., Fulton L.,
RA Garner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Smaildon N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sprat J., Woldman P.,
RT "2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Wamsley, P., Bradshaw H.;
RT "The sequence of C. elegans cosmid R10A10.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Waterston R.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U00449; AAB37826.1; -;
DR PIR: T29620; T29620.
DR HSSP: P28980; 1CHC.
DR WormRep: R10A10.2; CH12670.
DR InterPro: IPR001526; LY6_UPAR.
DR InterPro: IPR001841; ZnF_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00983; LY6_UPAR; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 112 AA; 12871 MW; 8F797E10FB701092 CRC64;

Query Match 43.2%; Score 266; DB 5; Length 112;
Best Local Similarity 41.3%; Pred. No. 3.2e-24;
Matches 45; Conservative 20; Mismatches 32; Indels 12; Gaps 2;
DB 1 MAAMVDPFGSGTNSGAGKKR-----FEVKNNVAVLWMDIVDNCALCRNHIMDL 52
1 MANSNADSGEGSTAKQKXTANPSRPVLKKNVAVLWMDIVDNCALCRVHLMBE 60

QY 53 CIECQANQASATSECTVAVGVCVCHAFHFCISRMKTRQVCPDNNREW 101
DB 61 CLRCQ-----SEPSAEVCVWGDCHHSFHHCCMTQWIKQNNRCPLQCKDW 105

RESULT 8

ID Q940X6 PRELIMINARY; PRT; 84 AA.
AC Q940X6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Anaphase promoting complex subunit 11.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Euxoicidae; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Okresz L.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AY052402; AAL13436.1; -;
DR InterPro: IPR001841; ZnF_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KM Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 84 AA; 9766 MW; 049678FED95882D6 CRC64;

Query Match 34.1%; Score 210; DB 10; Length 84;
Best Local Similarity 38.6%; Pred. No. 1.3e-17;
Matches 34; Conservative 18; Mismatches 26; Indels 8; Gaps 3;

QY 21 REVKNNVAVLWMDIVDNCALCRNHIMDLCECQANQASATSECTVAVGVCVCHAFH 80
DB 2 KYKILWHAVAWMTDADETCGICRMVFDGCCPDCK-----LPDDCPLTWGACNHAH 56
QY 81 FHCISRMKTRQVCPDNNREWEFOX 105
DB 57 LHCILKWNVSQTQAHCPWCRREWFKE 84

RESULT 9

ID Q8H306 PRELIMINARY; PRT; 84 AA.
AC Q8H306;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Putative anaphase promoting complex subunit 11.
GN P0710F09.24
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
clone:P0710F09.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP005325; BAC21540.1; -;
DR InterPro: IPR001841; ZnF_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 84 AA; 9676 MW; 5CF99B1E32D5E09A CRC64;

Query Match 32.1%; Score 198; DB 10; Length 84;
Best Local Similarity 34.5%; Pred. No. 3.7e-16;
Matches 34; Conservative 18; Mismatches 26; Indels 8; Gaps 3;

Matches 30; Conservative 20; Mismatches 29; Indels 8; Gaps 2;

QY 21 REFVKNNAVALMADIVDNCALICRNHIMDLCECQANQASATSEECTVAMGVCHNAFFH 80
 Db 2 KYKILQMGVAVSWNNADGTGICRNAPFDGCCPCCK-----FEDDDCLPMGVCSCNAPFH 56
 QY 81 FHCISRLMKTR---OVCPUDNREWEFQ 104
 Db 57 LHCILKMNVSOTSTPLCCPCRCREMOFK 83

RESULT 10

QYVLJ5 PRELIMINARY; PRT; 85 AA.
 AC QYVLJ5; QYVLJ4;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE CG18042 protein (putative Apc11 anaphase-promoting complex subunit).
 DE LMG OR CG18042.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Abril J.F., Doyle C., Baxter S.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Wan K.H., Abghyani A., An H.-Y., Andrews-Pfankuch C., Baldwin D.,
 RA Ballow R.M., Basu A.V., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu L.E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fodor C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Golder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lesko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy U., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Slater E., Spalding A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J., Q.A.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celnikier S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Bazzon J., An H., Baldwin D., Beeson K.Y., Busam D.A.,

RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegam C., Jalali M., Kruse D., Li P., Matei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacle J.M., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
 RT "Sequencing of Drosophila melanogaster genome";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[3]
 RP SEQUENCE FROM N.A.
 RA Maier S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochman S.B., Smith C.D.,
 RA Tupy J.L., Bergman C., Bertram B., Carlson J.W., Celnikier S.E.,
 RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Milburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
 RT "Annotation of Drosophila melanogaster genome";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celnikier S.E., Gibbs R.A., Rubin G.M., Venter J.C.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[5]
 RP SEQUENCE FROM N.A.
 RA Flybase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

[6]
 RP SEQUENCE FROM N.A.
 RA Taylor C.A., Shitras A.D.;
 RT "Cell cycle arrest and apoptosis in lemming mutants of Drosophila melanogaster";
 RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE003621; AA052694.2;
 DR EMBL; AJ251510; CAB63945.1;
 DR FLYbase; FB00029004; lmg.
 DR InterPro; IPR001841; Znf ring.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 SQ SEQUENCE 85 AA; 9859 MW; 01EF449D32BEDBA2 CRC64;

Query Match 32.0%; Score 197; DB 5; Length 85;
 Best Local Similarity 37.3%; Pred. No. 5e-16;
 Matches 31; Conservative 13; Mismatches 31; Indels 8; Gaps 2;

QY 24 VKKNNNAVALMADIVDNCALICRNHIMDLCECQANQASATSEECTVAMGVCHNAFFH 83
 Db 5 IKSWGVATWVWINDNCGICRNSFSTCEC-----ALPGDDCLPMGVCSCNAPFH 59

QY 84 ISRWLKTROV---CPUDNREWEF 103
 Db 60 IYKWLNLQPLNKQCPMCRQSWKF 82

RESULT 11

ID Q8IC8 PRELIMINARY; PRT; 89 AA.

AC Q8IC8;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Anaphase-promoting complex subunit, putative.

GN MAL6P1.184.

OS Plasmodium falciparum (Isolate 3D7).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

NCBI_TaxID=36329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cherevach I., Davis P., Goodhead I., Stevens K., Mungall K.,
 RA Bertram M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,

RA Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrett B.,
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL844505; CAD50514.1; -;
DR InterPro: IPR001841; Znf_ring;
DR PROSITE: PSS0089; ZF_RING_2; 1;
SQ SEQUENCE 89 AA; 10211 MW; 987493D9583BA23D CRC64;

Query Match 24.5%; Score 151; DB 5; Length 89;
Best Local Similarity 33.3%; Pred. No. 1.8e-10;
Matches 28; Conservative 16; Mismatches 32; Indels 8; Gaps 4;

QY 24 VKKNAVALMAM-DIVVDN-CALGRNHMDLCECOANQASATSECTVAMGVCHNAFPH 81
DB 6 VKRIHAARFWMKISTSDSCALCNSSLENTTTCM-----RPNCGCPAFGKCHHFL 60

QY 82 HCISRWLKTQGV-CPDNRREWEFQ 104
DB 61 HCMKMKIKONKLTCCCRADWYE 84

RESULT 12

Q20052 PRELIMINARY; PRT; 135 AA.
ID Q20052
AC Q20052
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE F35G12.9 protein.
GN F35G12.9.
OS Caenorhabditis elegans.
OC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;
OC Rhabdilitida; Pelodermidae; Caenorhabditis.
OX NCBI_Taxid=6239;

RA [1]
RP SEQUENCE FROM N.A.
RA Chui C.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=95069613; PubMed=9851916;
RA MEDLINE=95069613; PubMed=9851916;

RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
RT Science 282:2012-2018 (1998).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: Z46242; CAA86328.1; -;
DR PIR: T21802; T21802
DR WormPep: F35G12.9; CE00978.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SMO0184; RING; 1.
DR PROSITE: PSS0089; ZF_RING_2; 1.
KW Metal-binding; zinc; zinc-finger.

SQ SEQUENCE 135 AA; 15512 MW; 1CC8B4AFLAB671E7 CRC64;

Query Match 23.8%; Score 146.5; DB 5; Length 135;
Best Local Similarity 33.3%; Pred. No. 1e-09;
Matches 28; Conservative 10; Mismatches 35; Indels 11; Gaps 3;

QY 24 VKKNAVALMAM-DIVVDNCAICRNHMDLCECOANQASATSECTVAMGVCHNAFPH 82
DB 53 VKKLHVGEMKMLQGGEDTCGICMFEBSAC-----NNCKKFGDDCPVLGICRHAFFRH 107

QY 83 CISRWL-----KTRQVCPDNRREW 101
DB 108 CIDKWIAPFNPRAQCPDNRDW 131

RESULT 13

Q20052 PRELIMINARY; PRT; 57 AA.
ID Q20052
AC Q20052
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE F10A16.17 protein.
GN F10A16.17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;

RA [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ev. Columbia;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
RA Roming C.M., Koo H., Fujii C.Y., Uterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC F10A16 genomic sequence."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AC013393; AAF26089.1; -;
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SMO0184; RING; 1.
DR PROSITE: PSS0089; ZF_RING_2; 1.
KW Metal-binding; zinc; zinc-finger.

SQ SEQUENCE 57 AA; 6580 MW; 504C75B7B745C74 CRC64;

Query Match 22.9%; Score 141; DB 10; Length 57;
Best Local Similarity 41.1%; Pred. No. 1.8e-09;
Matches 23; Conservative 12; Mismatches 13; Indels 8; Gaps 3;

QY 53 CIECOANQASATSECTVAMGVCHNAFPHCISRWL--KTRQV-CPDNRREWEFQ 105
DB 7 CPDCK-----LPDGDCCPLIWGACNHAFFHLICLKWNSQTSQAHCPGRREWEFQ 57

RESULT 14
Q2157 PRELIMINARY; PRT; 165 AA.
ID Q2157
AC Q2157
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chromosome IV reading frame ORF YDL008W.
GN APC11 OR D2800 OR YDL008W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_Taxid=4932;

RA [1]
RP SEQUENCE FROM N.A.
RA Urestrazu L.A., Andre B., Viessers S.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RX SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RX SEQUENCE FROM N.A.
RC STRAIN=ALPHA 5288C;
RA Andre B., Viessers S., Urestrazu L.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z74056; CAA98564.1; -;
DR EMBL: Z48432; CAA86351.1; -;
DR PIR: S52511; S52511.
DR SGD: S0002166; APC11.
DR GO: GO:0004842; Fubidgulin-protein ligase activity; IDA.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SMO0184; RING; 1.
DR PROSITE: PSS0089; ZF_RING_2; 1.
KW Hypothetical protein.

SQ SEQUENCE 165 AA; 18865 MW; 99F8B8C6B841934 CRC64;

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 25, 2004, 09:25:22 ; Search time 17 Seconds
(without alignments)
330.739 Million cell updates/sec

Title: US-09-914-324A-1

Perfect score: 616
Sequence: 1 MAAMDVDPGSGTNSGAGK.....KTRQVCPIDNREMFQKXGH 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	616	100.0	108	1 RBX1_HUMAN	Q96288 homo sapien
2	614	98.1	108	1 RBX1_SALSA	Q86964 salmo salar
3	534	86.7	108	1 RBXA_DROME	Q94061 drosophila
4	514.5	83.5	118	1 RBXA_ARATH	Q940X7 arabidopsis
5	499	81.0	115	1 RBXB_ARATH	Q940B0 arabidopsis
6	493	80.0	110	1 RBX1_CAEL	Q23457 caenorhabdi
7	469	76.1	107	1 RBX1_SCHPO	Q13959 schizosacch
8	400.5	65.0	122	1 RBXB_DROME	Q91X00 drosophila
9	385	62.5	121	1 RBX1_YEAST	Q08273 saccharomyc
10	292	47.4	113	1 RBX2_HUMAN	Q9UBF6 homo sapien
11	290.5	47.2	113	1 RBX2_MOUSE	Q9WCX9 mus musculu
12	209	33.9	84	1 ANI1_MOUSE	Q9N9X5 homo sapien
13	208	33.8	84	1 ANI1_HUMAN	Q9N9X5 homo sapien
14	164.5	26.7	94	1 YTP3_SCHPO	Q9N986 schizosacch
15	91	14.8	148	1 RN24_HUMAN	Q9N925 homo sapien
16	90	14.6	600	1 RN12_MOUSE	Q9N9V7 mus musculu
17	88	14.3	161	1 YODU_CAEL	P30631 caenorhabdi
18	87	14.1	624	1 RN12_HUMAN	Q9N9W2 homo sapien
19	86	14.0	326	1 PEXA_HUMAN	Q06083 homo sapien
20	85.5	13.9	232	1 RBX1_HUMAN	Q9Y415 homo sapien
21	83.5	13.6	115	1 YBR2_YEAST	P38823 saccharomyc
22	83	13.5	685	1 RNPF_HUMAN	Q9N952 homo sapien
23	82.5	13.4	532	1 ICP0_HSVB	P26903 equine herp
24	80	13.0	284	1 GOL1_DROME	Q06003 drosophila
25	79.5	12.9	305	1 Z364_MOUSE	Q960C1 mus musculu
26	79.5	12.9	796	1 PRH_ARATH	P48785 arabidopsis
27	79	12.8	381	1 RN13_CHICK	Q940Z2 gallus gall
28	79	12.8	381	1 RN13_HUMAN	Q43567 homo sapien
29	79	12.8	410	1 ICP0_PVIF	P29129 pseudorabie
30	79	12.8	583	1 YOF7_SCHPO	Q9N971 schizosacch
31	79	12.8	1679	1 FUR2_DROME	P30432 drosophila
32	78.5	12.7	225	1 YQ57_CAEL	Q09463 caenorhabdi
33	78	12.7	381	1 RN13_MOUSE	Q54565 mus musculu

34	77	12.5	279	1	SL13_HUMAN	Q14192 homo sapien
35	77	12.5	295	1	PEXA_PICAN	Q09340 picnia angu
36	76.5	12.4	643	1	AMP2_HUMAN	Q9UKV5 homo sapien
37	76.5	12.4	643	1	AMP2_MOUSE	Q9UKV5 mus musculu
38	76.5	12.4	758	1	YK04_YEAST	P36096 saccharomyc
39	75	12.3	1493	1	M3K1_MOUSE	P53349 mus musculu
40	75	12.3	1493	1	M3K1_RAT	Q62825 rattus norv
41	76	12.3	1493	1	M3K1_HUMAN	Q13233 homo sapien
42	75.5	12.3	676	1	ICP0_HSVB	P29128 bovine herp
43	75.5	12.3	676	1	ICP0_HSVB	P29128 bovine herp
44	74.5	12.1	825	1	ICP0_HSV2H	P28284 herpes simp
45	74	12.0	474	1	CBLC_HUMAN	Q9U1V8 homo sapien

ALIGNMENTS

RESULT 1
ID RBX1_HUMAN STANDARD; PRT; 108 AA.
AC Q96288; Q9DLS2; Q9WUK3; Q9Y254;
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE RING-box protein 1 (Rbx1) (Regulator of cullins 1) (RING finger protein 75) (ZYP protein).
DE RBX1 OR ROCI OR RNF75.
GN Homo sapiens (Human), and
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606, 10090;
RN [1]
RP SEQUENCE FROM N.A., INTERACTION WITH CULLINS, AND MUTAGENESIS OF CY5-53; CY5-56; CY5-75 AND HIS-77.
RC SPECIES=Human; TISSUE=Cervical carcinoma;
RX MEDLINE=99247022; PubMed=10230407;
RA Ohta T., Michel J.J., Schottelius A.J., Xiong Y., "ROCI, a homolog of APC1, represents a family of cullin partners with an associated ubiquitin ligase activity.", Mol. Cell 3:535-541(1999).
RL [2]
RN SEQUENCE FROM N.A., AND IDENTIFICATION IN CBC(VHL) COMPLEX.
RP SPECIES=Human, and Mouse;
RC MEDLINE=99234320; PubMed=10233691;
RX Kanura T., Koepf D.M., Conrad M.N., Skowrya D., Moreland R.J., Iliopoulos O., Lane W.S., Kaelin W.G. Jr., Ellledge S.J., Conway R.C., Harper J.W., Conway J.W., "Rbx1, a component of the VHL tumor suppressor complex and SCF ubiquitin ligase.", Science 284:657-661(1999).
RL [3]
RN SEQUENCE FROM N.A.
RP SPECIES=Human;
RC MEDLINE=20057165; PubMed=10591208;
RX Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M., Clump M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K., Bagshaw C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J., Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Conway D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E., Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Evans K.L., Fey J.M., Fleming K., French L., Garner A.A., Gilbert J.G., Goward M.B., Graham D.V., Griffiths M.N.D., Hall C., Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A., Latrid G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M., Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T., McElay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T., Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,

RA Soderlund C., Spraggon L., Stewart C.A., Silston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Mochizuki S., Kaseaki K., Sasaki T., Asakawa S., Kudo Y.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuuma S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Hu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malat J., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren O., Shaili S., Sloan D., Song L.,
RA Man Q., Wang Y., Wang Z., White J., Williamson D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Zhao S., Murray J., Miller N., Min P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du J., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Laveille P., Layman D., Ozeresky P., Rohlfing T.,
RA Schreier P., Walker C., Wamley A., Wohldmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Salter S.,
RA Budarf M.L., McEneaney H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA Peyrard M., Kieda D., Seroussi E., Franssone L., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenleitch A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tlathun Y., Wright H.,
RT "The DNA sequence of human chromosome 22.",
RT Nature 402:489-495(1999).
[4]
RA SEQUENCE FROM N.A.
RA SPECIES=Human, and Mouse; TISSUE=Brain, Mammary gland, and Placenta;
RC MEDLINE=22386257; PubMed=12477932;
RX Strauberg R.L., Petingold E.A., Grouse L.H., Derge J.G.,
RA Alausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh F.,
RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Sepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toehiyuki S., Carrinzi P., Prange C.,
RA Rana S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska D.E.,
RA Scherch A., Schin J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences".
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RA SEQUENCE FROM N.A.
RA SPECIES=Mouse; STRAIN=C57BL/6J; TISSUE=Embryo;
RC MEDLINE=22354683; PubMed=12466851;
RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikiado I., Oate N., Saito R., Suzuki H., Yamakawa T., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quakechun J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Betzel K.W.,
RA Blake J.A., Brad T., Brusci V., Chochia C., Corbani L.E., Cousins S.,
RA Dalia E., Dragant T.A., Fletcher C.F., Forrest A., Frazier K.S.,
RA Gaesteland T., Gariboldi M., Gissi C., Goddik A., Gough J.,
RA Grimmond S., Gustinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Keldzierski P.M., King B.L.,
RA Kanaga A., Kurochkin I.V., Lee Y., Lemnath B., Lyons P.A.,
RA Maglott D.R., Maltas L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
RA Pavlovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shmida K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Mahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilting L.G., Wynshaw-Boris A., Yarnagisawa M., Yang I., Yang L.,
RA Yuan Z., Zevocian W., Zhu Y., Zimmer A., Carinici F., Hayatsu N.,
RA Hirozane-Kishikawa T., Kohno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yamashita A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs".
RT Nature 420:563-573(2002).
[6]
RA SEQUENCE OF 14-108 FROM N.A.
RA SPECIES=Human; TISSUE=Brain;
RC MEDLINE=20106778; PubMed=10643962;
RX Pater J.-P., Seddigi N., Charbonnier F., Goudou D., Belkadi L.,
RA Rieger F., Alliel P.M.,
RT "Genomic organization and expression of the ubiquitin-proteasome
complex-associated protein Rbx1/ROCI/Hrt1".
RT Cell. Mol. Biol. 45:1131-1137(1999).
[7]
RA SEQUENCE OF 92-105, INTERACTION WITH CUL1, AND
RA IDENTIFICATION IN A COMPLEX WITH CUL1, SKP1 AND SKP2.
RA SPECIES=Human; TISSUE=Cervical carcinoma;
RC MEDLINE=99247021; PubMed=10230406;
RX Tan P., Fuchs S.Y., Chen A., Wu K., Gomez C., Ronai Z., Pan Z.-Q.,
RT "Recruitment of a ROCI-CUL1 ubiquitin ligase by Skp1 and HOS to
catalyze the ubiquitination of I kappa B alpha".
RT Mol. Cell 3:527-533(1999).
[8]
RA FUNCTION.
RA SPECIES=Human;
RC MEDLINE=20047893; PubMed=10579999;
RX Kanura T., Conrad M.N., Van O., Conway R.C., Conway J.W.,
RT "The Rbx1 subunit of SCF and VHL E3 ubiquitin ligase activates Rbx1
modification of cullin Cdc53 and Cul2".
RT Genes Dev. 13:2928-2933(1999).
[9]
RA FUNCTION, AND SUBCELLULAR LOCATION.
RA SPECIES=Human;
RC MEDLINE=20481777; PubMed=11072288;
RX Furukawa M., Zhang Y., McCarthy J., Ohta T., Xiong Y.,
RT "The CUL1 C-terminal sequence and ROCI are required for efficient
nuclear accumulation, NED8 modification, and ubiquitin ligase
activity of CUL1".
RT Mol. Cell Biol. 20:8185-8197(2000).
[10]
RA IDENTIFICATION IN E3 UBIQUITIN LIGASE COMPLEX WITH MUF1, AND
RA IDENTIFICATION IN COMPLEXES WITH CUPS.
RA SPECIES=Human, and Mouse;
RC MEDLINE=21380117; PubMed=11384984;
RX Kamura T., Burian D., Yan Q., Schmidt S.L., Lane W.S., Querido E.,
RA Branton P.E., Shilatifard A., Conway R.C., Conway J.W.,
RT "Muf1, a novel Elongin BC-interacting leucine-rich repeat protein
that can assemble with CUPS and Rbx1 to reconstitute a ubiquitin
ligase".
RT J. Biol. Chem. 276:29748-29753(2001).
[11]
RA IDENTIFICATION IN E3 UBIQUITIN LIGASE COMPLEX WITH MED8.
RA SPECIES=Human;
RC MEDLINE=22155962; PubMed=12149480;
RX Brower C.S., Sato S., Tomomori-Sato C., Kamura T., Pause A.,
RA Steatman R., Klausner R.D., Malik S., Lane W.S., Sorokina I.,
RA Roeder R.G., Conway J.W., Conway R.C.,
RT "Mammalian mediator subunit MED8 is an Elongin BC-interacting protein
that can assemble with Cul2 and Rbx1 to reconstitute a ubiquitin
ligase".
RT Proc. Natl. Acad. Sci. U.S.A. 99:10353-10358(2002).
[12]
RA IDENTIFICATION IN SCF-LIKE COMPLEX, AND INTERACTION WITH CUL7.
RA SPECIES=Human;
RC MEDLINE=22388271; PubMed=12481031;
RX Dias D.C., Dolios G., Wang R., Pan Z.-Q.,
RT "CUL7: A DCC domain-containing cullin selectively binds Skp1, Fbx29 to
form an SCF-like complex".

Query Match 100.0%; Score 616; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 3,5e-61;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAMADVTPSGTNSGAGKRRFEVKKNVAMAMDIYVNCALCRNHIMDLCTEGCQANQ 60
 DB 1 MAAMADVTPSGTNSGAGKRRFEVKKNVAMAMDIYVNCALCRNHIMDLCTEGCQANQ 60

QY 61 ASATSECTVAMGVCMNAFFHCISRWLKTROVCPDLNREWEFOKYGH 108
 DB 61 ASATSECTVAMGVCMNAFFHCISRWLKTROVCPDLNREWEFOKYGH 108

RESULT 2
 RBX1 SALSA STANDARD; PRT; 108 AA.

AC 08064;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE RING-box protein 1 (Rbx1) (Hyperosmotic protein 21).
 GN RBX1 OR SHOP21.
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OC NCBI_TaxID=8030;
 RX MEDLINE=22005592; PubMed=12010746;
 RC TISSUE=G11;
 RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND INDUCTION.

RT "A homolog of the E3 ubiquitin ligase Rbx1 is induced during
 hyperosmotic stress of salmon."
 RL Am. J. Physiol. 282:R1643-R1653(2002).
 CC -1- FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) E3
 ubiquitin ligase complex, which mediates the ubiquitination and
 subsequent proteasomal degradation of target proteins. Through the
 RING-type zinc finger, seems to recruit the E2 ubiquitination
 enzyme, like CDC34, to the complex and brings it into close
 proximity to the substrate (By similarity).
 CC -1- PARTWAY: Ubiquitin conjugation; third step.
 CC -1- SUBUNIT: Part of SCF complexes, which consist of SKP1, CUL1,
 RBX1 and a F-box protein (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
 CC -1- TISSUE SPECIFICITY: Expressed in heart and kidney.
 CC -1- INDUCTION: During hyperosmotic stress and thermal stress.
 CC -1- DOMAIN: The RING-type zinc finger domain is essential for
 ubiquitin ligase activity. It coordinates an additional third zinc
 atom.
 CC -1- SIMILARITY: Belongs to the RBX1 family.

CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
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 or send an email to license@sib-sib.ch).

DR EMBL; AY027936; AA29182.1; ALT_INT.
 DR InterPro; IPR001841; Znf_11.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PSS0089; ZF_RING_2; 1.
 KW Ubl conjugation pathway; Nuclear protein; Zinc; Zinc-finger;
 KM Metal-binding.
 FT ZN FING 53 98 RING-TYPE
 FT METAL 42 42 ZINC 1 (BY SIMILARITY)
 FT METAL 45 45 ZINC 1 (BY SIMILARITY)
 FT METAL 53 53 ZINC 3 (BY SIMILARITY)

FT METAL 56 56 ZINC 3 (BY SIMILARITY)
 FT METAL 68 68 ZINC 2 (BY SIMILARITY)
 FT METAL 75 75 ZINC 2 (BY SIMILARITY)
 FT METAL 77 77 ZINC 2 (BY SIMILARITY)
 FT METAL 80 80 ZINC 1 (BY SIMILARITY)
 FT METAL 82 82 ZINC 3 (BY SIMILARITY)
 FT METAL 83 83 ZINC 1 (BY SIMILARITY)
 FT METAL 94 94 ZINC 2 (BY SIMILARITY)
 FT METAL 97 97 ZINC 2 (BY SIMILARITY)
 SQ SEQUENCE 108 AA; 12318 MM; 44GCEAV12CEDCTBB CR664;
 Query Match 98.1%; Score 604; DB 1; Length 108;
 Best Local Similarity 98.1%; Pred. No. 7,4e-60;
 Matches 106; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAAMADVTPSGTNSGAGKRRFEVKKNVAMAMDIYVNCALCRNHIMDLCTEGCQANQ 60
 DB 1 MAAMADVTPSGTNSGAGKRRFEVKKNVAMAMDIYVNCALCRNHIMDLCTEGCQANQ 60

QY 61 ASATSECTVAMGVCMNAFFHCISRWLKTROVCPDLNREWEFOKYGH 108
 DB 61 ASATSECTVAMGVCMNAFFHCISRWLKTROVCPDLNREWEFOKYGH 108

RESULT 3
 RBXA DROME STANDARD; PRT; 108 AA.

AC 09W5EL; 077429;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE RING-box protein 1A (Regulator of cullins 1a) (dRbx1).
 GN ROCI1A OR CG16982 OR EG:115C2.11.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RX MEDLINE=20196006; PubMed=10731132;
 RC STRAIN=Berkley;
 RP SEQUENCE FROM N.A.

RT Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amaratides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Berns P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Crawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D.A., Heiman T.O., Hernandez J.R., Houck J.,
 Hoston D., Houston K.A., Howland T.J., Wei M.-H., Idagham C.,
 Jaislin M., Kalush F., Karpen G.H., Ke Z., Kennison U.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Lasero P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Mishaeva N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Paclet J.M.,
 Palazzolo M., Plattman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,
 Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z., Wastaman D.A., Weinstein G.M., Weissensbach J.,
RA Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye Y., Yen R.-P., Zaveri U.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of *Drosophila melanogaster*,"
RL Science 287:2195-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Oregon-R;
RX MEDLINE=20196011; PubMed=10731137;
RA Benos P.V., Galt M.K., Ashburner M., Murphy L., Harris D.,
RA Barrett B.G., Ferraz C., Vidal S., Brun C., Demallies J., Cadieu E.,
RA Dreesen S., Gloux S., Lelure V., Mottler S., Galibert F., Borikova D.,
RA Mirana B., Kafatos F.C., Louis C., Siden-Klamos E., Bolshakov S.,
RA Papagannakis G., Spanos L., Cox S., Madueno E., de Pablo S.,
RA Modolli J., Peter A., Schoettler P., Werner M., Moutikoti F.,
RA Belmont N., Dowe G., Schefer U., Jaekle H., Bucketon A.,
RA Callister D.M., Campbell L.A., Parlatitsou A., Henderson N.S.,
RA McWilliam P.D., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
RA Glover D.M.;
RT "From sequence to chromosome: the tip of the X chromosome of *D.*
RT *melanogaster*,"
RL Science 287:2220-2222(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely; TISSUE=Embryo;
RX MEDLINE=22426066; PubMed=12537569;
RA Stepleton M., Carlson J.W., Brokstein P., Yu C., Champagne M.,
RA George R.A., Garlin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A *Drosophila* full-length cDNA resource,"
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.6(2002).
RN [4]
RP FUNCTION, TISSUE SPECIFICITY, DEVELOPMENTAL STAGE, AND MUTAGENESIS OF
RP ASN-59 AND CYS-68.
RX MEDLINE=22057626; PubMed=12062088;
RA Nureiddine M.A., Donaldson T.D., Thacker S.A., Duronio R.J.;
RT *Drosophila* Roca encodes a RING-H2 protein with a unique function in
RT processing the Hb signal transducer Ci by the SCF E3 ubiquitin
RT ligase.";
RL Dev. Cell 2:757-770(2002).
RN [5]
RP INTERACTION WITH LIN19 AND SIMB.
RX MEDLINE=21391618; PubMed=11500045;
RA Bocca S.N., Muzzapappa M., Silberstein S., Wapner P.;
RT "Occurrence of a putative SCF ubiquitin ligase complex in
RT *Drosophila*,"
RL Biochem. Biophys. Res. Commun. 266:357-364(2001).
RN [6]
RP REVIEW ON E3 UBIQUITIN LIGASE COMPLEXES.
RX MEDLINE=22736111; PubMed=12850443;
RA Ou C.-Y., Pi H., Chen C.-T.;
RT "Control of protein degradation by E3 ubiquitin ligases in *Drosophila*
RT eye development,";
RL Trends Genet. 19:382-389(2003).
RN [7]
RP FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) E3
RP ubiquitin ligase complex, which mediates the ubiquitination and
RP subsequent proteasomal degradation of target proteins through the
RP RING-type zinc finger, seems to recruit the E2 ubiquitin
RP enzyme to the complex and brings it into close proximity to the
RP substrate. Required for the specific SCF-dependent proteolysis of
RP Ci, but not that of ANM, suggesting that it also participates in
RP the selection of substrates inside the SCF complex.
RN [8]
RP PATHWAY: Ubiquitin conjugation; third step.
RN [9]
RP SUBUNIT: Part of a SCF complex consisting of SkpA (SKP1), Lin19
RP (CUL1), RocA and F-box protein Simb. Interacts directly with
RN [10]
RP SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
RN [11]
RP TISSUE SPECIFICITY: Widely expressed. Expressed in embryonic,
RN [12]
RP larval and adult tissues.
RN [13]
RP DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
RN [14]
RP DOMAIN: The RING-type zinc finger domain is essential for

```

CC ubiquitin ligase activity. It coordinates an additional third zinc atom (By similarity).
CC -1- SIMILARITY: Belongs to the RING-box family.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous gene model prediction.
CC -----
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CC -----
DR EMBL; AE003418; AAF45536.1; ALT_SEQ.
DR EMBL; AL031581; CAA20888.1; -.
DR EMBL; AY119265; AAM51125.1; -.
DR PIR; T13388; T13388.
DR FlyBase; FBgn0025638; Rcc1a.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00097; zf-C3HC4_1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Ub1 conjugation pathway; Nuclear protein; Developmental protein; Zinc; Zinc-finger; Metal-binding.
FT DN FING 53 98
FT FT POLY-SER.
FT METAL 12 15
FT METAL 42 42 ZINC 1 (BY SIMILARITY).
FT METAL 45 43 ZINC 1 (BY SIMILARITY).
FT METAL 53 53 ZINC 1 (BY SIMILARITY).
FT METAL 56 56 ZINC 3 (BY SIMILARITY).
FT METAL 68 68 ZINC 3 (BY SIMILARITY).
FT METAL 75 75 ZINC 2 (BY SIMILARITY).
FT METAL 77 77 ZINC 2 (BY SIMILARITY).
FT METAL 80 80 ZINC 1 (BY SIMILARITY).
FT METAL 82 82 ZINC 3 (BY SIMILARITY).
FT METAL 83 83 ZINC 1 (BY SIMILARITY).
FT METAL 94 94 ZINC 2 (BY SIMILARITY).
FT METAL 97 97 ZINC 2 (BY SIMILARITY).
FT MUTAGEN 59 59 N->C; LOSS OF FUNCTION WHEN ASSOCIATED WITH R-68.
FT FT C->R; LOSS OF FUNCTION WHEN ASSOCIATED WITH C-59.
SQ SEQUENCE 108 AA; 12538 MW; 15784198281BCD13 CRC64;
Query Match 86.7%; Score 534; DB 1; Length 108;
Best Local Similarity 87.2%; Pred. No. 3.9e-52;
Matches 95; Conservative 4; Mismatches 4; Indels 6; Gaps 2
QY MDVD-----TSQGSGAGKRFVEYKKNNVAALWMDIVDNCAICRNHIMDLCEQQAN 59
DB 1 MEVDDGGEVSESSSKG-DKRFEYKKNNVAALWMDIVDNCAICRNHIMDLCEQQAN 59
QY QASATSECTVAMGVGNFAFHFCISRLTKTRQVCPLNRRREMRFGKH 108
DB 60 QASATSECTVAMGVGNFAFHFCISRLTKTRQVCPLNRRREMRFGKH 108
DB 60 QASATSECTVAMGVGNFAFHFCISRLTKTRQVCPLNRRREMRFGKH 108
RESULT 4
REXA_ARATH STANDARD; PRT; 118 AA.
AC Q94OX7;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE RING-box protein 1a (RBX1a-Ac) (Ac-Rbx1;1) (RBX1-2).
GN RBX1A OR ARS50570 OR PTCH.160.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliopsida; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxId=3702;
RN [1]

```


FT METAL 104 104 ZINC 2 (BY SIMILARITY)
 FT METAL 107 107 ZINC 2 (BY SIMILARITY)
 SO SEQUENCE 118 AA; 13238 MM; 13947BF06F442A2 CRC64;
 Query Match 83.5%; Score 514.5; DB 1; Length 118;
 Best Local Similarity 78.6%; Pred. No. 6.1e-50;
 Matches 92; Conservative 6; Mismatches 8; Indels 11; Gaps 2;

QY 3 AAMVDVTPSG-----TNSGAGKREVKKNVAVLWMDIVDNCALCRNHND 51
 DB 2 ATLSDVTMIRAGENASSVVAASNNKAKREIKKMSAVLWMDIVDNCALCRNHND 61
 QY 52 LCIECOANQASATSEECTVANGVGNHAFHFCISRMKTKTQVCPDNDREWEFOKYG 108
 DB 62 LCIECOANQASATSEECTVANGVGNHAFHFCISRMKTKTQVCPDNDREWEFOKYG 118

RESULT 5
 RXB_XAPATH STANDARD; PRT; 115 AA.
 AC 09M2B0;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Putative RING-box protein 1b (RBX1b-Ac) (At-RBX1.2) (RBX1-1).
 GN RBX1B OR AT3G42830 OR T21C14.50.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxID=3702;
 RX SEQUENCE FROM N.A.
 RP STRAIN=cv. Columbia;
 RC MEDLINE=21016720; PubMed=11130713;
 RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unselid M.,
 RA Fatmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
 RA Delaney M., Boutry M., Griwall L.A., Macho R., Pulgomech P.,
 RA De Simone V., Cholsne N., Artiguenave F., Robert C., Broclet P.,
 RA Winkler P., Catalicio L., Weisenbach J., Saurin W., Queirer F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs N., Beres V.,
 RA Wurmach E., Drzonek H., Exfle H., Jordan N., Bangert S.,
 RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
 RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
 RA Reinhardt U., Schaefer M., Schoen O., Bagnies M., Terol J., Clement J.,
 RA Navarro P., Collado C., Perez-Perez A., Oltenswelder B., Duchemin D.,
 RA Cooke R., Laude M., Berger-Liauz J.-P., Collet A., Casacuberta E.,
 RA De Haan M., Maere A.C., Alcaraz J., P., Cortes A., Casacuberta E.,
 RA Montfort A., Argitrou A., Flores M., Liguori R., Vitale D.,
 RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walts R., Wu D., Peterson J., Van Aken S.,
 RA Cressy T.H., Haas B., Walts R., Wu D., Peterson J., Van Aken S.,
 RA Pal G., Miltscher U., Sellers P., Gill J.E., Feldhym T.V.,
 RA Preuss D., Lin X., Nieman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Frazer C.M., Kaneo T., Nakamura Y., Sato S., Kato T., Asamizu E.,
 RA Sasamoto S., Kimura T., Idegawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa S., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Matanabe A., Yamada M., Yasuda M., Tabata S.;
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 thaliana.";
 RL Nature 408:820-822 (2000).
 RN
 RP DISCUSSION OF SEQUENCE.
 RX MEDLINE=2204438; PubMed=12215511;
 RA Gray W.M., Hellmann H., Dharmasiri S., Estelle M.;
 RT "Role of the Arabidopsis RING-H2 protein RBX1 in RUB modification and
 SCF function.";
 RL Plant Cell 14:2137-2144 (2002).
 RN
 RP TISSUE SPECIFICITY.

RX MEDLINE=22370998; PubMed=12381738.
 RA Lechner E., Xie D., Grava S., Pigaglio E., Planchais S., Shen W.-H.,
 RA Murray J.A.H., Parmentier Y., Mutterer J., Dubreucq B., Shen W.-H.,
 RA Genschik P.;
 RT "The AtRBX1 protein is part of plant SCF complexes, and its
 down-regulation causes severe growth and developmental defects.";
 RL J. Biol. Chem. 277:50063-50068 (2002).
 CC -1- FUNCTION: Potential component of the SCF (SKP1-CUL1-F-box protein)
 CC E3 ubiquitin ligase complex, which mediates the ubiquitination and
 CC subsequent proteasomal degradation of target proteins. The SCF
 CC complex plays a crucial role in regulating response to auxin and
 CC is essential for growth and development. Through the RING-type
 CC zinc finger, seems to recruit the E2 ubiquitination enzyme, to the
 CC complex and brings it into close proximity to the substrate (By
 CC similarity).
 CC -1- PATHWAY: Ubiquitin conjugation; third step.
 CC -1- SUBUNIT: Potential part of SCF complexes, which consist of a SKP1-
 CC related protein, a cullin, a RBX protein and a F-box protein.
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic (By similarity).
 CC -1- TISSUE SPECIFICITY: Not detected in floral buds, stems and roots.
 CC -1- DOMAIN: The RING-type zinc finger domain is essential for
 CC ubiquitin ligase activity. It coordinates an additional third zinc
 CC atom.
 CC -1- SIMILARITY: Belongs to the RBX1 family.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
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 CC
 DR EMBL: AT138633; CAB87200.1; -
 DR PIR: T47341; T47341;
 DR InterPro: IPR001841; Znf_Ring.
 DR Pfam: PF00097; Zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Hypothetical protein; Ub1 conjugation pathway; Nuclear protein; Zinc;
 KW Zinc-finger; Metal-binding.
 FT ZN_FING 60 107
 FT METAL 49 49
 FT METAL 52 52
 FT METAL 60 60
 FT METAL 63 63
 FT METAL 75 75
 FT METAL 84 84
 FT METAL 87 87
 FT METAL 89 89
 FT METAL 90 90
 FT METAL 101 101
 FT METAL 104 104
 SO SEQUENCE 115 AA; 12999 MM; 1515E3B41VDB1FAF CRC64;

QY 1 MAAMPVDVTPSGTNSGAGKREVKKNVAVLWMDIVDNCALCRNHNDICICQANO 60
 DB 10 MGSSSSISVPS--SSSKNSRFFELKMSAVLWMDIVDNCALCRNHNDICICQANO 67
 QY 61 ASATSEECTVANGVGNHAFHFCISRMKTKTQVCPDNDREWEFOKYG 108
 DB 68 ASATSEECTVANGVGNHAFHFCISRMKTKTQVCPDNDREWEFOKYG 115
 RESULT 6
 RBX1_CABEL STANDARD; PRT; 110 AA.
 ID RBX1_CABEL

Thu Mar 25 10:42:33 2004

us-09-914-324a-1.rsp

Page 7

AC Q23457; Q8WSQ1; 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE RING-box protein 1 (Rbx1) (Ce-rbx-1).
 GN RBX-1 OR ZK287.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Felodermatidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Brictol N2;
 RA McMurray A.A.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE OF 2-110 FROM N.A.
 RA Sasagawa Y., Urano T., Kohara Y., Takahashi H., Higashitani A.;
 RT "Characterization of rbx1 gene from Caenorhabditis elegans."
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) E3
 CC ubiquitin ligase complex, which mediates the ubiquitination and
 CC subsequent proteasomal degradation of target proteins. Through the
 CC RING-type zinc finger, seems to recruit the E2 ubiquitination
 CC enzyme to the complex and brings it into close proximity to the
 CC substrate (By similarity).
 CC -1- PATHWAY: Ubiquitin conjugation; third step.
 CC -1- SUBUNIT: Part of SCF complexes, which consist of a SKP1 or a SKP1-
 CC related protein, a cullin protein, and a F-box protein (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
 CC -1- DOMAIN: The RING-type zinc finger domain is essential for
 CC ubiquitin ligase activity. It coordinates an additional third zinc
 CC atom.
 CC -1- SIMILARITY: Belongs to the RING-box family.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-10 is the initiator.
 CC
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 CC
 CC EMBL; Z70757; CAA94801.1; -
 CC EMBL; AB07287; BAB83695.1; ALT_INTT.
 CC PIR; T27823; T27823.
 CC WormBep; ZK287.5; CE06614.
 CC InterPro; IPR001841; Znf_Ring.
 CC Pfam; PF00097; ZF-C3HC4; 1.
 CC SMART; SM00184; RING; 1.
 CC PROSITE; PSS00089; ZF_RING_2; 1.
 CC K1M Ub1 conjugation pathway; Nuclear protein; Zinc; Zinc-finger;
 CC Metal-binding.
 CC
 CC FT ZN RING 44 100 RING-TYPE.
 CC FT METAL 44 44 ZINC 1 (BY SIMILARITY).
 CC FT METAL 47 47 ZINC 3 (BY SIMILARITY).
 CC FT METAL 55 55 ZINC 3 (BY SIMILARITY).
 CC FT METAL 58 58 ZINC 3 (BY SIMILARITY).
 CC FT METAL 70 70 ZINC 2 (BY SIMILARITY).
 CC FT METAL 77 77 ZINC 2 (BY SIMILARITY).
 CC FT METAL 79 79 ZINC 2 (BY SIMILARITY).
 CC FT METAL 82 82 ZINC 1 (BY SIMILARITY).
 CC FT METAL 84 84 ZINC 3 (BY SIMILARITY).
 CC FT METAL 85 85 ZINC 1 (BY SIMILARITY).
 CC FT METAL 96 96 ZINC 2 (BY SIMILARITY).
 CC FT METAL 99 99 ZINC 2 (BY SIMILARITY).
 CC FT CONFLICT 2 3 AQ -> GP (IN REF. 2).
 CC SQ SEQUENCE 110 AA; 12760 MW; EFES0F7664B30A56 CRC64;

Query Match 80.0%; Score 493; DB 1; Length 110;

Best Local Similarity 79.3%; Pred. No. 1.3e-47;
 Matches 88; Conservative 5; Mismatches 14; Indels 4; Gaps 2;
 OY 1 MAAMP---VDTSNGNSGAGKREFEVKTMNVAVLAMPDIYDNCALICRHHMDLCIECO 57
 DB 1 MAQASSTAMEVEATNQTV-KRFEVKRMSAVLAMPDIYDNCALICRHHMDLCIECO 59
 OY 58 ANQASATSECTVAMGVCMNAFFPHFCISRWLKTQVCPLDNRWEPQKXGH 108
 DB 60 ANQASAGKDECTVAMGNCHNAFFPHFCISRWLKTQVCPLDNRWEPQKXGH 110
 RESULT 7
 RBX1 SCHPO STANDARD; PRT; 107 AA.
 AC 013959;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE RING-box protein p1p1 (Pop-interacting protein 1) (RING-box protein
 DE 1).
 GN P1P1 OR SPAC23H4.18C.
 OS Schizosaccharomyces pombe (Fission Yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.; FUNCTION, SUBCELLULAR LOCATION, AND INTERACTION
 RP WITH POP1, POP2 AND PCUL1.
 RX MEDLINE=22325333; PubMed=2167173;
 RA Seibert V., Prohl C., Schultze I., Rhee E., Lopez R., Abderazzag K.,
 RA Zhou C., Wolf D.A.;
 RT "Combinatorial diversity of fission yeast SCF ubiquitin ligases by
 RT home- and heterooligomeric assemblies of the F-box proteins Pop1p and
 RT Pop2p."
 RL BMC Biochem. 3:22-22(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21849401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles D., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Falgout T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Wungaili K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Wolckardt G., Aert R., Robben J., Gymnopoulos B.,
 RA Welljens I., Vansireels E., Rieger M., Schneider M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leinrich H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambut R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Ulmenz J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
 RA "The genome sequence of Schizosaccharomyces pombe."
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: Component of E3 ubiquitin ligase SCF complexes, which
 CC mediate the ubiquitination and subsequent proteasomal degradation
 CC of target proteins. Seems to recruit the E2 ubiquitination enzyme,
 CC like UBC3/CDC34, to the complex and brings it into close proximity
 CC to the substrate.
 CC -1- PATHWAY: Ubiquitin conjugation; third step.

CC -1- SUBUNIT: Part of a SCF E3 ubiquitin ligase complex containing
 CC psh1, pip1, pull1 and the F-box proteins pop1 and pop2. Instead of
 CC the pop1/pop2 heterodimer also homooligomers of pop1 or pop2 may
 CC be present in the complex.
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -1- DOMAIN: The RING-type zinc finger domain is essential for
 CC ubiquitin ligase activity. It coordinates an additional third zinc
 CC atom.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF192228; AAD54393.1; -
 DR PIR; T38310; T38310.
 DR GeneDB; SPombe; SPAC23H4.18c; -
 DR InterPro; IPR001841; Znf_fing.
 DR Pfam; PF00097; Zf-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KM ubi conjugation pathway; Nuclear protein; Zinc; Zinc-finger;
 KM Metal-binding.
 FT ZN FING 52 97 RING-TYPE.
 FT METAL 41 41 ZINC 1 (BY SIMILARITY).
 FT METAL 44 44 ZINC 1 (BY SIMILARITY).
 FT METAL 52 52 ZINC 3 (BY SIMILARITY).
 FT METAL 55 55 ZINC 3 (BY SIMILARITY).
 FT METAL 67 67 ZINC 3 (BY SIMILARITY).
 FT METAL 74 74 ZINC 2 (BY SIMILARITY).
 FT METAL 76 76 ZINC 2 (BY SIMILARITY).
 FT METAL 79 79 ZINC 1 (BY SIMILARITY).
 FT METAL 81 81 ZINC 3 (BY SIMILARITY).
 FT METAL 82 82 ZINC 1 (BY SIMILARITY).
 FT METAL 93 93 ZINC 2 (BY SIMILARITY).
 FT METAL 96 96 ZINC 2 (BY SIMILARITY).
 SQ SEQUENCE 107 AA; 12724 MW; 71C3A3D2BF26DABF CRC64;

Query Match 76.1%; Score 469; DB 1; Length 107;
 Best Local Similarity 87.5%; Pred. No. 5.8e-45;
 Matches 77; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 21 REVKKKNAVALMADIYVNCALCRNIMIDLCICQANQASATSECTVAMGVONAFH 80
 DB 20 REIKKKNAVALMWDIVDNCALGRNIMIDLCICQANTSPAAQECTVAMGVONAFH 79
 QY 81 FHCISRWLTQVCPIDNREWEFOYKGG 108
 DB 80 FHCISRWLTQVCPIDNREWEFOYKGG 107

RESULT 8
 REBX DROME STANDARD; FRT; 122 AA.
 ID REBX DROME STANDARD; FRT; 122 AA.
 AC Q9NHX0; Q9W0R1;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE RING-box protein 1B (Regulator of cullins 1b).
 GN RING-BOX OR RING-BOX OR CG16988.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Rhyngroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION AND TISSUE SPECIFICITY.
 MDLINE=22057626; PubMed=12062088;

RA Nouredine M.A., Donaldson T.D., Thacker S.A., Duronio R.U.;
 RT "Drosophila Roca encodes a RING-H2 protein with a unique function in
 RT processing the Hb signal transducer Ci by the SCF E3 ubiquitin
 RT ligase.";
 RL Dev. Cell 2:757-770(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amaralides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bandaru D., Bolshakov S.,
 RA Borzova D., Botchan M.R., Bouck H., Cadieu E., Center A., Chandra I.,
 RA Burris K.C., Buesen D.A., Butler H., Caden E., Davies P.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson R., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Idegawa C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison U.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson A.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
 RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Rhue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,
 RA Stryker R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan W., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley; TISSUE=Testis;
 RX MEDLINE=22426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Garin H., Krommiller B., Pauley J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celisner S.E.;
 RT "A Drosophila full-length cDNA resource.";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 CC -1- FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) E3
 CC ubiquitin ligase complex, which mediates the ubiquitination and
 CC subsequent proteasomal degradation of target proteins. Through the
 CC RING-type zinc finger, seems to recruit the E2 ubiquitination
 CC enzyme to the complex and brings it into close proximity to the
 CC substrate (By similarity).
 CC -1- PATHWAY: Ubiquitin conjugation; third step.
 CC -1- SUBUNIT: Part of a SCF complex consisting of SkpA (SKP1),
 CC Ltn19 (CUL1), Roc1a and a F-box protein (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Highly expressed in early embryos, and in
 CC pupae. Widely expressed in adult males, while it is weakly
 CC expressed in adult females.
 CC -1- DOMAIN: The RING-type zinc finger domain is essential for
 CC ubiquitin ligase activity. It coordinates an additional third zinc
 CC atom (By similarity).
 CC -1- SIMILARITY: Belongs to the RING-box family.

CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -1- CAUTION: It is uncertain whether Met-1 or Met-16 is the initiator.
CC -----
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CC -----
DR EMBL: AF218290; AAF32313.1; ALT_INIT.
DR EMBL: AE003468; AAF47382.1; -.
DR EMBL: AY070810; AAL48432.1; -.
DR FLYBASE: FBgn0040291; Rocl.b.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF000097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Ubl conjugation pathway; Nuclear protein; Zinc; Zinc-finger;
KW Metal-binding.
FT ZN FING 57 112 RING-TYPE.
FT METAL 68 68 ZINC 3 (BY SIMILARITY).
FT METAL 71 71 ZINC 3 (BY SIMILARITY).
FT METAL 82 82 ZINC 3 (BY SIMILARITY).
FT METAL 96 96 ZINC 3 (BY SIMILARITY).
FT METAL 57 57 ZINC 1 (BY SIMILARITY).
FT METAL 60 60 ZINC 1 (BY SIMILARITY).
FT METAL 89 89 ZINC 2 (BY SIMILARITY).
FT METAL 91 91 ZINC 2 (BY SIMILARITY).
FT METAL 94 94 ZINC 1 (BY SIMILARITY).
FT METAL 97 97 ZINC 1 (BY SIMILARITY).
FT METAL 108 108 ZINC 2 (BY SIMILARITY).
FT METAL 111 111 ZINC 2 (BY SIMILARITY).
SQ SEQUENCE 122 AA; 14225 MW; F22CE00438725410 CR664;
Query Match 65.0%; Score 400.5; DB 1; Length 122;
Best Local Similarity 65.4%; Pred. No. 2.4e-37;
Matches 70; Conservative 13; Mismatches 19; Indels 5; Gaps 2;
QY 5 MVDYDPSGNGSG---AGKREYKKNVAALAMADIVDNCAIRNIMDLCECOAQ 60
DB 16 MGFNNEPSCSGAVARTERFVKKVAHAWMGWDVAVDNCALRNHIMLCECOAD 74
QY 61 ASATSECTVAVGVCHAFPHICISRWLKTROVCEPLDREMEFQKYG 107
DB 75 PHANQDECTVANGCHNAFHHCIAWLTIRLVCPIDNKEMWYQKYG 121
RESULT 9
REX1 YEAST STANDARD; PRT; 121 AA.
ID REX1 YEAST 008273;
AC 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE RING-box protein HRT1 (RING-box protein 1).
DE HRT1 OR REX1 OR YOL131W.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
OX NCBI_TaxId=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8288C / FY1679;
RX MEDLINE=97051593; PubMed=8896270;
RA Aldela M., Piedrafita L., Casas C., Casamayor A., Khalid H.,
RA Balcells L., Arino J., Herrero B.,
RT "Sequence analysis of a 12 801 bp fragment of the left arm of yeast
RT chromosome XV containing a putative 6-phosphofructo-2-kinase gene, a
RT gene for a possible glycoprophospholipid-anchored surface protein and
RT six other open reading frames.";
RT Yeast 12:1053-1058(1996).
RN [2]
RP SEQUENCE OF 8-31, FUNCTION, INTERACTION WITH CDC53, CDC4 AND
RP CDC34, AND IDENTIFICATION IN SCF COMPLEX.
RX MEDLINE=99315634; PubMed=10385629;
RA Seol J.H., Feldman R.M.R., Zachariae W., Shevchenko A., Correll C.C.,
RA Iyavarna S., Chi Y., Galova M., Claypool J., Sandmeyer S., Naemly K.,
RA Shevchenko A., Deshaies R.J.;
RT "Cdc3/cullin and the essential Hrt1 RING-H2 subunit of SCF define a
RT ubiquitin ligase module that activates the E2 enzyme Cdc34.";
RT Genes Dev. 13:1614-1626(1999).
RN [3]
RP IDENTIFICATION IN SCF COMPLEX, INTERACTION WITH CDC34 AND CDC4, AND
RP MUTANT REX1-1.
RX MEDLINE=99234321; PubMed=10213692;
RA Skowrya D., Koepf D.M., Kamura T., Conrad M.N., Conaway R.C.,
RA Conaway U.W., Blledge S.J., Harper J.W.;
RT "Reconstitution of G1 cyclin ubiquitination with complexes containing
RT SCFgr1 and Rbx1.";
RT Science 284:662-665(1999).
RN [4]
RP FUNCTION.
RX MEDLINE=20047893; PubMed=10579999;
RA Kamura T., Conrad M.N., Yan Q., Conaway R.C., Conaway J.W.;
RT "The Rbx1 subunit of SCF and VHL E3 ubiquitin ligase activates Rbx1
RT modification of cullins Cdc53 and Cul2.";
RT Genes Dev. 13:2928-2933(1999).
RN [5]
RP SUBCELLULAR LOCATION AND MUTANT HRT1-C81Y.
RX MEDLINE=20341308; PubMed=10880467;
RA Blondel M., Galan U.-W., Peter M.;
RT "Isolation and characterization of HRT1 using a genetic screen for
RT mutants unable to degrade Gic2p in Saccharomyces cerevisiae.";
RT Genetics 155:1033-1044(2000).
CC -1- FUNCTION: Component of E3 ubiquitin ligase SCF complexes, which
CC mediate the ubiquitination and subsequent proteasomal degradation
CC of target proteins. Seems to recruit the E2 ubiquitination enzyme,
CC like UBC3/CDC34, to the complex and brings it into close proximity
CC to the substrate. Also stimulates UBC3/CDC34 autoubiquitination
CC and promotes the neddylation of CDC53.
CC -1- PATHWAY: Ubiquitin conjugation; third step.
CC -1- SUBUNIT: Part of SCF E3 ubiquitin ligase complexes containing
CC CBF3, CDC53, HRT1 and F-box proteins YJL149W or GR1. Interacts
CC with CDC53, CDC4 and UBC3.
CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC -1- DOMAIN: The RING-type zinc finger domain is essential for
CC ubiquitin ligase activity.
CC -1- SIMILARITY: Belongs to the RING-box family.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -1- CAUTION: It is uncertain whether Met-1 or Met-8 is the initiator.
CC -----
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CC -----
DR EMBL: X93465; CA64737.1; -.
DR EMBL: Z74876; CA89155.1; -.
DR PIR: S66830; S66830.
DR SGD: S0005493; HRT1.
DR GO: GO:0005737; C:cytoplasm; IDA.
DR GO: GO:0005634; C:nucleus; IDA.
DR GO: GO:0005315; F:protein binding; IPI.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IDA.
DR InterPro: IPR001841; Znf_ring.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Ubl conjugation pathway; Nuclear protein; Zinc; Zinc-finger;
KW Metal-binding.
FT ZN FING 55 111 RING-TYPE.
FT METAL 55 55 ZINC 1 (BY SIMILARITY).

FT METAL 58 58 ZINC 1 (BY SIMILARITY)
 FT METAL 66 66 ZINC 3 (BY SIMILARITY)
 FT METAL 69 69 ZINC 3 (BY SIMILARITY)
 FT METAL 81 81 ZINC 3 (BY SIMILARITY)
 FT METAL 88 88 ZINC 2 (BY SIMILARITY)
 FT METAL 90 90 ZINC 2 (BY SIMILARITY)
 FT METAL 93 93 ZINC 1 (BY SIMILARITY)
 FT METAL 95 95 ZINC 1 (BY SIMILARITY)
 FT METAL 96 96 ZINC 1 (BY SIMILARITY)
 FT METAL 107 107 ZINC 2 (BY SIMILARITY)
 FT METAL 110 110 ZINC 2 (BY SIMILARITY)
 FT MUTAGEN 72 72 K-S: IN RBX1-1; TEMPERATURE SENSITIVE
 FT MUTAGEN 81 81 ALLELE. AT 38 DEGREES CELSIUS INDUCES
 FT MUTAGEN 81 81 DEFECTS IN UBIQUITIN LIGASE ACTIVITY WHEN
 FT MUTAGEN 81 81 ASSOCIATED WITH R-81.
 FT MUTAGEN 81 81 C-S: IN RBX1-1; TEMPERATURE SENSITIVE
 FT MUTAGEN 81 81 ALLELE. AT 38 DEGREES CELSIUS INDUCES
 FT MUTAGEN 81 81 DEFECTS IN UBIQUITIN LIGASE ACTIVITY WHEN
 FT MUTAGEN 81 81 ASSOCIATED WITH R-72.
 FT MUTAGEN 81 81 C-S: IN HRT1-C81Y; DEFECTS IN UBIQUITIN
 FT MUTAGEN 81 81 LIGASE ACTIVITY.
 FT SEQUENCE 121 AA; 13940 MW; A9C3193E46CAF861 CRC64;
 SO SEQUENCE 121 AA; 13940 MW; A9C3193E46CAF861 CRC64;
 Query March 62.5% Score 385; DB 1; Length 121;
 Best Local Similarity 56.6% Pred. No. 1,2e-35;
 Matches 64; Conservative 10; Mismatches 29; Indels 10; Gaps 1;
 5 MDVDPISGTSNAG-----KKREVKKNNAVALMWDIVDNCATCRHINDLCT 54
 8 MDVDEDSQNIQAQSNQSAPEVETKKRFEIKMTAVAFWMSDIAVNCALCRHIMEPCI 67
 55 ECGANQASATSEECTVAVGVCNNAHFHFCISRMKTQVCLNDREMEPOKYG 107
 68 ECGPRAMTDITNECVAMGVCHAFHLCINKIKINDACPLDQNPQRLARCG 120

RT Mol. Cell. Biol. 19:3145-3155(1999).
 RP [4] SEQUENCE FROM N.A. (ISOFORM 2).
 RP MEDLINE=21398045; PubMed=11506706;
 RX Swaroop M., Goshik M., Sun Y.,
 RT "SAG/ROC2/Rbx2/Hrt2, a component of SCF E3 ubiquitin ligase: genomic
 RT structure, a splicing variant, and two family pseudogenes";
 RT DNA Cell Biol. 20:425-434(2001).
 RP [5] SEQUENCE FROM N.A. (ISOFORM 1).
 RP Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
 RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
 RA Phelan M., Farmer A.;
 RT "Cloning of human full-length cDNAs in BD Creator(TM) system donor
 RT vector";
 RT Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 RP [6] SEQUENCE FROM N.A. (ISOFORM 1).
 RP TISSUE=Brain, and Kidney;
 RP MEDLINE=22389257; PubMed=12477932;
 RX Strausberg R.L., Pelngold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapelton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lottellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosa S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Holys S.W.,
 RA Villalon D.K., Wozny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schultz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP [7] INTERACTION WITH CUL1, AND FUNCTION.
 RP MEDLINE=20309864; PubMed=10851089;
 RX Swaroop M., Wang Y., Miller P., Duan H., Jackie T., Madore S.J.,
 RA Sun Y.;
 RT "Yeast homolog of human SAG/ROC2/Rbx2/Hrt2 is essential for cell
 RT growth, but not for germination: chip profiling implicates its role
 RT in cell cycle regulation";
 RT Oncogene 19:2855-2866(2000).
 RP [8] PHOSPHORYLATION BY CK2.
 RP MEDLINE=22765395; PubMed=12748192;
 RX Kim Y.-S., Lee J.-Y., Son M.-Y., Park W., Bae Y.-S.;
 RT "Phosphorylation of chreonine 10 on CKBp1/SAG/ROC2/Rbx2 by protein
 RT kinase CKII promotes the degradation of IkappaBalpha and p27kip1";
 RT J. Biol. Chem. 278:28462-28469(2003).
 RP [9] FUNCTION: Probable component of the SCF (SKP1-CUL1-F-box protein)
 RP E3 ubiquitin ligase complex which mediates the ubiquitination and
 RP subsequent proteasomal degradation of target proteins involved in
 RP cell cycle progression, signal transduction and transcription.
 RP Through the RING-type zinc finger, seems to recruit the E2
 RP ubiquitination enzyme to the complex and brings it into close
 RP proximity to the substrate. May play a role in protecting cells
 RP from apoptosis induced by redox agents.
 RP [10] PATHWAY: Ubiquitin conjugation; third step.
 RP [11] SUBUNIT: Probable part of SCF complexes, which consist of SKP1,
 RP CUL1, RNF7/Rbx2 and a F-box protein. Interacts with CUL1, CUL2,
 RP CUL3, CUL4A, CUL4B and CUL5. Interacts with CSNK2B, the
 RP interaction is not affected by phosphorylation by CK2.
 RP [12] SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
 RP [13] ALTERNATIVE PRODUCTS:
 RP Event=Alternative splicing; Named isoforms=2;
 RP Name=1;

CC IsoId=Q9UBF6-1; Sequence=Displayed;
CC Name=2; Synonyms=SAG-V;
CC IsoId=Q9UBF6-2; Sequence=VSP_008449;
CC Note=inactive;
CC TISSUE SPECIFICITY: Expressed in heart, liver, skeletal muscle and
CC pancreas. At very low levels expressed in brain, placenta and
CC lung.
CC INDUCTION: By 1,10-phenanthroline.
CC DOMAIN: The RING-type zinc finger domain is essential for
CC ubiquitin ligase activity. It coordinates an additional third zinc
CC atom.
CC FUNCTION: Phosphorylation by CK2 is required for efficient degradation
CC of NFkBIA and CDKN1B.
CC SIMILARITY: Belongs to the RING-box family.
CC SIMILARITY: Contains 1 RING-type zinc finger.
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DR EMBL: ARI64679; AAD5984.1; -
DR EMBL: ARI42860; AAD30147.1; -
DR EMBL: AF092878; AAD25962.1; -
DR EMBL: AF112262; AAK37450.1; -
DR EMBL: BT007348; AAP36012.1; -
DR EMBL: BC005966; AAH05966.1; -
DR EMBL: BC008627; AAH08627.1; -
DR MIM: 603863; -
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR SMART: SMO0184; RING; 1.
DR PROSITE: PSS0089; ZF_RING_2; 1.
KW Ub1 conjugation pathway; Zinc; Zinc-finger; Metal-binding;
KW Phosphorylation; Alternative splicing.
FT ZN FING 61 103
FT METAL 50 50
FT METAL 53 53
FT METAL 61 61
FT METAL 64 64
FT METAL 73 73
FT METAL 80 80
FT METAL 82 82
FT METAL 85 85
FT METAL 87 87
FT METAL 88 88
FT METAL 99 99
FT METAL 102 102
FT MOD RES 10 10
FT VASAPLIC 60 113

FT ACACGAKNCOEDCVVWVGKNSFHNCKMSLWVKNRRCP
FT LCQCDWVYGRIG -> EGIQVWMSALNLINASEGRCF
FT RSGSTALAVPSVSLASHQPCLDHHR (in isoform 2).
FT /FTId=VSP_008449.
FT K -> T (in REF. 2).
SQ CONFLICT 23 23
SEQUENCE 113 AA; 12683 MM; CE1E6CAC940C8257 CRC64;

Query March 47.4%; Score 292; DB 1; Length 113;
Best Local Similarity 50.5%; Pred. No. 2.1e-25;
Matches 49; Conservative 14; Mismatches 30; Indels 4; Gaps 2;

QY 11 SGTNSGAKRPFVEYKNAVALWMDIVDNCALCRNHINDLCTEQANQASATSECTV 70
DB 20 SGRSGG-GDKWFSIKKNAVAMWSMVDVCDTCALCRVQWADACLRCAEN---KQEDCVV 75
QY 71 AWGVCNNAFHHCISRLKTKTQVCPIDNREMEPKYK 107
DB 76 VMGECNHSFHNCKMSLWVKNRRCPCLCOQDWVVRIG 112

RESULT 11

RBX2 MOUSE
ID RBX2 MOUSE STANDARD; PRT; 113 AA.
AC Q9WTZ1;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE RBX2 protein 2 (RBX2) (RING finger protein 7) (sensitive to
DE apoptosis gene protein).
GN RN7 OR RBX2 OR SAG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Lung;
RX MEDLINE=99182502; PubMed=10082581;
RA Duan H., Wang Y., Aviram M., Swaroop M., Loo J.A., Bian J., Tian Y.,
RA Mueller T., Bisgaier C.L., Sun Y.;
RT "SAG, a novel zinc RING finger protein that protects cells from
RT apoptosis induced by redox agents";
RL Mol. Cell. Biol. 19:3145-3153(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L.M., Strubli F., Suzuki R., Tomita M., Wagner L., Masnio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G.,
RA Blake J., Botelli D., Bojuna N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Butt C., Fletcher M., Hume D.A., Kamuya M., Lee N.H.,
RA Guestincin S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Haegawa Y., Kawai H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Casavant T.M., Schetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.M., Schetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshitsuki S., Carinci P., Prange C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McManus P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiy S.W.,
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy E., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC FUNCTION: Probable component of the SCF (SKP1-CUL1-F-box protein) and
CC E3 ubiquitin ligase complex which mediates the ubiquitination of
CC subsequent proteasomal degradation of target proteins involved in

```

CC cell cycle progression, signal transduction and transcription.
CC Through the RING-type zinc finger, seems to recruit the E2
CC ubiquitination enzyme to the complex and brings it into close
CC proximity to the substrate. May play a role in protecting cells
CC from apoptosis induced by redox agents.
CC -1- PATHWAY: Ubiquitin conjugation; third step.
CC -1- SUBUNIT: Probable part of SCF complexes, which consist of SKP1,
CC CUL1, RNF7/RBX2 and a F-box protein. Interacts with CUL1, CUL2,
CC CUL3, CUL4A, CUL4B, CUL5 and CSXK2B (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -1- DOMAIN: The RING-type zinc finger domain is essential for
CC ubiquitin ligase activity. It coordinates an additional third zinc
CC atom.
CC -1- SIMILARITY: Belongs to the RING-box family.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF092877; AAD25961.1; -
CC EMBL: AF0013248; BAB22666.1; -
CC EMBL: AK001127; AAH1127.1; -
CC MGI: MGI1337096; Rnf7.
CC GO: GO:0005737; C:cytoplasm; IDA.
CC GO: GO:0005634; C:nucleus; IDA.
CC GO: GO:0006916; P:anti-apoptosis; IDA.
CC GO: GO:0008637; P:apoptotic mitochondrial changes; IDA.
CC GO: GO:0006919; P:caspase activation; IDA.
CC GO: GO:0008631; P:induction of apoptosis by oxidative stress; IDA.
CC InterPro: IPR001841; Znf_ring.
CC Pfam: PF00097; ZF-C3HC4_1.
CC SMART: SM00184; RING_1.
CC PROSITE: PS50089; ZF_RING_2; 1, Zinc-finger, Metal-binding.
CC KX Ubl conjugation pathway; Zinc; Zinc-finger, Metal-binding.
CC ZN FING 61 103
CC METAL 50 50
CC METAL 53 53
CC METAL 61 61
CC METAL 64 64
CC METAL 73 73
CC METAL 80 80
CC METAL 82 82
CC METAL 85 85
CC METAL 87 87
CC METAL 88 88
CC METAL 99 99
CC METAL 102 102
CC SEQUENCE 113 AA, 12707 MW, D6FA02BE6038FDD2 CRC64;
CC -----
CC Query Match 47.2%; Score 290.5; DB 1; Length 113;
CC Best Local Similarity 44.8%; Pred. No. 3e-25; 35; Indels 13; Gaps 3
CC Matches 52; Conservative 16; Mismatches -----
CC QY 1 MAAPADVDPR-----SGTNSGAGKRFYKKNNAYALWAMDIVDNCAICRNHND 51
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 1 MADVEDGEPRCVLSSHSGSAGRSQ-GDMFSLKKNNAYALWMSDVECTCAICRYQVND 59
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC DB 52 LCIEQANQASATSECTVANGVCHNAHFHFCISRLKTRQVCPDLNREMEPKYQ 107
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 60 AGLRCQAEH--KQEDCVVWAGECNHSFHNCCMSLWVKQNNRCPCLCQGDWVYQRIQ 112
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC -----
CC RESULT 12
CC ID AN11_MOUSE STANDARD; PRT; 84 AA.
CC Q9CRF9; Q9CTG0; 40, Created)
CC 16-OCT-2001 (Rel. 40, Last sequence update)
CC 16-OCT-2001 (Rel. 40, Last sequence update)

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DR EMBL; BC000607; AAH00607.1; -
DR Genem; HGNC:14452; ANAPC11.
DR GK; G9NYG5; -
DR InterPro; IPR001841; Znf_ring.
DR SMART; SM00184; RING_1; Znf_ring.
DR PROSITE; PS50089; ZF_RING_2; 1.
KM Ubl conjugation pathway; Cell cycle; Cell division; Mitosis; Zinc;
KM Zinc-finger; Metal-binding; Nuclear protein; Ubl conjugation;
KM Alternative splicing.
FT ZN FING 34 77 RING-TYPE.
FT METAL 23 23 ZINC 1 (BY SIMILARITY).
FT METAL 26 26 ZINC 1 (BY SIMILARITY).
FT METAL 34 34 ZINC 3 (BY SIMILARITY).
FT METAL 37 37 ZINC 3 (BY SIMILARITY).
FT METAL 44 44 ZINC 3 (BY SIMILARITY).
FT METAL 51 51 ZINC 2 (BY SIMILARITY).
FT METAL 53 53 ZINC 2 (BY SIMILARITY).
FT METAL 56 56 ZINC 1 (BY SIMILARITY).
FT METAL 58 58 ZINC 3 (BY SIMILARITY).
FT METAL 59 59 ZINC 1 (BY SIMILARITY).
FT METAL 73 73 ZINC 2 (BY SIMILARITY).
FT METAL 76 76 ZINC 2 (BY SIMILARITY).
FT VARSPLIC 1 37 MKVKKICMGVATLWVANDENCGICRMFNGCCPDC ->
/Flid=VSP 008450.
FT MUTAGEN 23 23 C->S: GREATLY REDUCES AUTOUBIQUITINATION
FT MUTAGEN 26 26 C->S: GREATLY REDUCES AUTOUBIQUITINATION
FT MUTAGEN 34 34 C->S: SLIGHTLY REDUCES AUTOUBIQUITINATION
FT MUTAGEN 37 37 C->S: SLIGHTLY REDUCES AUTOUBIQUITINATION
FT MUTAGEN 44 44 C->S: SLIGHTLY REDUCES AUTOUBIQUITINATION
FT MUTAGEN 51 51 C->S: GREATLY REDUCES AUTOUBIQUITINATION
FT MUTAGEN 53 53 H->S: GREATLY REDUCES AUTOUBIQUITINATION
FT MUTAGEN 56 56 H->S: GREATLY REDUCES AUTOUBIQUITINATION
FT MUTAGEN 58 58 H->S: SLIGHTLY REDUCES AUTOUBIQUITINATION
FT MUTAGEN 59 59 C->S: GREATLY REDUCES AUTOUBIQUITINATION
FT MUTAGEN 73 73 C->S: GREATLY REDUCES AUTOUBIQUITINATION
FT MUTAGEN 76 76 C->S: GREATLY REDUCES AUTOUBIQUITINATION
FT SEQUENCE 84 AA; 9841 MW; EACGBSAB4FDCL1AE CRC64;
SQ
Query Match 33.8%; Score 208; DB 1; Length 84;
Best Local Similarity 37.5%; Pred. No. 2.8e-16;
Matches 33; Conservative 17; Mismatches 30; Indels 8; Gaps 2;

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OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=2184901; PubMed=11859360;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagers K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymptre B.,
RA Melchens I., Vantrevels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moesli D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Furnelle B.,
RA Goffeau A., Cadieu E., Driano S., Gloux S., Lelaire V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Rhode G.,
RA Dama R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Bento J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
RA Cerutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PR745; PubMed=9501991;
RX MEDLINE=98162722; PubMed=9501991;
RA Yoshida S., Kato K., Nakai K., Okayama H., Nojima H.,
RT "Identification of open reading frames in Schizosaccharomyces pombe
RT cDNA."
RL DNA Res. 4:363-369 (1997).
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
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CC or send an email to license@sdb.ch).
CC -----
DR EMBL; AL109739; CAB52266.1; -
DR EMBL; AB001022; BA19216.1; ALT_SEQ.
DR PIR; T38652; T38652.
DR GenBank; Spombe; SPAC343.03; -
DR InterPro; IPR001841; Znf_ring.
DR SMART; SM00184; RING_1; Znf_ring.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
KM Hypothetical protein; Zinc-finger.
FT ZN FING 35 78 RING-TYPE.
FT SEQUENCE 94 AA; 10557 MW; C770021339C3626 CRC64;
SQ
Query Match 26.7%; Score 164.5; DB 1; Length 94;
Best Local Similarity 33.7%; Pred. No. 2e-11;
Matches 28; Conservative 16; Mismatches 30; Indels 9; Gaps 3;

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QY 80 HFFHCISRWLKT---ROYCPDNR 99
 DB 57 HAHCIQWNLATSGSQGCCPDNRQ 79

RESULT 15

RN24 HUMAN STANDARD: PRT: 148 AA.

AC Q9Y225; Q9YH01; Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE RING finger protein 24.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_TaxId=9606;
 [1]

RP SEQUENCE FROM N.A. PubMed=11780052;

RA MEDLINE=21638749; PubMed=11780052;
 RA DeJours F., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark R.E., Connor R.E., Corby N.R.,
 RA Clegg S., Cobley V.E., Collier R.E., Dami P.D., Dunn M.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Gillingham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Lehaeslajho M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McIay K., McMurtry A.A.,
 RA Milne S.A., Misty D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaidin M., Wall M., Wallis J.W.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871 (2001).

RN [2]

RP SEQUENCE FROM N.A. PubMed=12477932;

RA MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Steinmetz M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,
 RA Villalon D.K., Murty D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [3]

RP SEQUENCE OF 45-148 FROM N.A.
 RA Basal M.T., Banfi S., Raboni M., Ballabio A., Boreani G.,
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC - SIMILARITY: Contains 1 RING-type zinc finger.
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DR EMBL, AL096778; CAB46627.1; -
 DR EMBL, AL031670; CAB43182.1; -
 DR EMBL, BC000213; AAH00213.1; -
 DR EMBL, BC039584; AAH39584.1; -
 DR EMBL, AL079313; CAB45279.1; -
 DR HSSP, P28930; ICRC.
 DR Genew; HGNC:13779; RNF24.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00097; ZF_C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS0089; ZF_RING_2; 1.
 KW Zinc-finger.
 FT ZN-FING 78 119
 FT ZN-FING 45 45
 FT CONFLICT 45 45 Y->S (IN REF. 3).
 SO SEQUENCE 148 AA; 17209 MW; 66C240C3A591EAS CRC64;

QY 75 CNAHFFHCISRWLKTROYCPDNR 98
 DB 96 CKHAFRKLKWLKLVKVCPLCN 119
 Query Match 14.8%; Score 91; DB 1; Length 148;
 Best Local Similarity 58.3%; Pred. No. 0.0041;
 Matches 14; Conservative 4; Indels 0; Gaps 0;

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 Job time: 17 secs

Thu Mar 25 10:42:33 2004

us-09-914-324a-1.rapb

Page 1

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OM protein - protein search, using sw model

Run on: March 25, 2004, 09:36:13 ; Search time 41 Seconds
(without alignments)
689,255 Million cell updates/sec

Title: US-09-914-324A-1

Perfect score: 616
Sequence: 1 MAAMVDVTPSGTNSGAGKK.....KTRQVCPDNRMEFQKXGH 108

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1065169 seqs, 26161801 residues

Total number of hits satisfying chosen parameters: 1065169

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Published Applications AA.*
2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	616	100.0	108	9	US-09-826-312-6
2	616	100.0	108	14	US-10-108-767-6
3	616	100.0	108	14	US-10-152-156-6
4	518.5	84.2	118	12	US-10-424-599-148916
5	506.5	82.2	152	12	US-10-424-599-221431
6	420.5	68.3	106	12	US-10-424-599-148915
7	313	50.8	75	12	US-10-424-599-230014
8	292	47.4	118	9	US-09-764-864-826
9	292	47.4	118	9	US-09-764-864-1285
10	287	46.6	64	12	US-10-424-599-228320
11	287	46.6	113	9	US-09-826-312-8
12	287	46.6	113	14	US-10-108-767-8
13	287	46.6	113	14	US-10-152-156-8
14	282	45.8	68	12	US-10-424-599-242288
15	228	37.0	40	12	US-10-424-599-264079

16	213	34.6	88	12	US-10-276-774-2678	Sequence 2678, Ap
17	213	34.6	88	14	US-10-102-806-520	Sequence 620, App
18	213	34.6	91	15	US-10-264-049-4937	Sequence 2937, Ap
19	213	34.6	105	9	US-09-764-864-1274	Sequence 1274, Ap
20	210	34.1	124	9	US-09-764-864-1284	Sequence 1284, Ap
21	208	33.8	84	12	US-10-221-625-94	Sequence 94, Appl
22	208	33.8	100	12	US-10-424-599-253860	Sequence 253860, Ap
23	202	32.8	84	9	US-09-826-312-5	Sequence 5, Appl
24	202	32.8	84	14	US-10-108-767-5	Sequence 5, Appl
25	202	32.8	84	14	US-10-152-156-5	Sequence 226, Ap
26	196	31.8	85	15	US-10-264-049-2926	Sequence 839, App
27	185.5	30.1	121	9	US-09-764-864-839	Sequence 839, App
28	185.5	30.1	121	9	US-09-764-864-1294	Sequence 1294, Ap
29	185.5	30.1	121	10	US-09-764-891-4639	Sequence 4639, Ap
30	175	28.4	73	12	US-10-424-599-235108	Sequence 235108, Ap
31	172	27.9	114	15	US-10-320-797-3003	Sequence 3003, Ap
32	138	22.4	34	12	US-10-424-599-254645	Sequence 254645, Ap
33	134.5	21.8	133	14	US-10-032-585-7259	Sequence 2589, Ap
34	102	16.6	144	12	US-10-424-599-279773	Sequence 279773, Ap
35	100.5	16.3	205	12	US-10-424-599-213911	Sequence 213911, Ap
36	98	15.9	234	12	US-10-424-599-266133	Sequence 266133, Ap
37	97.5	15.8	128	12	US-10-424-599-202979	Sequence 202979, Ap
38	97.5	15.8	195	12	US-10-425-114-16967	Sequence 36967, A
39	97.5	15.8	209	12	US-10-425-114-41999	Sequence 41999, A
40	97.5	15.8	209	12	US-10-425-114-63173	Sequence 63173, A
41	96.5	15.7	345	12	US-10-425-114-71489	Sequence 71489, A
42	96.5	15.7	356	12	US-10-424-599-179820	Sequence 179820, A
43	95.5	15.5	100	12	US-10-424-599-254121	Sequence 254121, A
44	95.5	15.5	202	12	US-10-424-599-254121	Sequence 254121, A
45	95.5	15.5	344	12	US-10-424-599-143394	Sequence 143394, A

ALIGNMENTS

RESULT 1
US-09-826-312-6
Sequence 6, Application US/09826312
Patent No. US20020042083A1
GENERAL INFORMATION:
APPLICANT: Iseakani, Sarkiz D.
APPLICANT: Huang, Jialie
APPLICANT: Sheng, Jialie
TITLE OF INVENTION: US/QUITTIN LIGASE ASSAY
FILE REFERENCE: A-68613-1/RMS/JCD
CURRENT APPLICATION NUMBER: US/09/826,312
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 09/542,497
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
US-09-826-312-6

Query Match 100.0% Score 616; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAMVDVTPSGTNSGAGKREYKNAVALMWDIVDNCACRNHINDICCOANQ 60
DB 1 MAAMVDVTPSGTNSGAGKREYKNAVALMWDIVDNCACRNHINDICCOANQ 60
QY 61 ASATSECTVAVGVCNHAFFHCISRMUKTROVCPDNRMEFQKXGH 108
DB 61 ASATSECTVAVGVCNHAFFHCISRMUKTROVCPDNRMEFQKXGH 108
RESULT 2
US-10-108-767-6

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; Sequence 6, Application US/10108767
; Publication No. US2003010447A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jiating
; APPLICANT: Sheng, Julie
; APPLICANT: Pray, Todd R.
; TITLE OF INVENTION: ASSAYS FOR IDENTIFYING UBIQUITIN AGENTS AND FOR IDENTIFYING AGENT
; TITLE OF INVENTION: MODIFY THE ACTIVITY OF UBIQUITIN AGENTS
; FILE REFERENCE: A-68613-5/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/108,767
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 10/091,139
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-767-6

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Query Match          100.0%; Score 616; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAAMDVTPSGTSGAGKRFKNNVAVLWMDIVDNCACRHHNDLCTECQANQ 60
DB 1 MAAMDVTPSGTSGAGKRFKNNVAVLWMDIVDNCACRHHNDLCTECQANQ 60

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QY 61 ASATSECTVAMGVGNHAFHFCISRWLKTROVCPDLNREWEFOKYGH 108
DB 61 ASATSECTVAMGVGNHAFHFCISRWLKTROVCPDLNREWEFOKYGH 108

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RESULT 3
US-10-152-156-6
; Sequence 6, Application US/10152156
; Publication No. US20030108947A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jiating
; APPLICANT: Sheng, Julie
; APPLICANT: Pray, Todd R.
; TITLE OF INVENTION: ASSAYS FOR IDENTIFYING UBIQUITIN AGENTS AND FOR IDENTIFYING AGENT
; TITLE OF INVENTION: MODIFY THE ACTIVITY OF UBIQUITIN AGENTS
; FILE REFERENCE: A-68613-6/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/152,156
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 10/091,174
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 10/091,139
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 10/109,460
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 10/108,767
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/291,836
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-152-156-6

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Query Match          100.0%; Score 616; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAAMDVTPSGTSGAGKRFKNNVAVLWMDIVDNCACRHHNDLCTECQANQ 60
DB 1 MAAMDVTPSGTSGAGKRFKNNVAVLWMDIVDNCACRHHNDLCTECQANQ 60

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QY 61 ASATSECTVAMGVGNHAFHFCISRWLKTROVCPDLNREWEFOKYGH 108
DB 61 ASATSECTVAMGVGNHAFHFCISRWLKTROVCPDLNREWEFOKYGH 108

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RESULT 4
US-10-424-599-148916
; Sequence 148916, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 148916
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_105494C.1.pep
US-10-424-599-148916

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Query Match          84.2%; Score 518.5; DB 12; Length 118;
Best Local Similarity 80.3%; Pred. No. 9.1e-50;
Matches 94; Conservative 5; Mismatches 7; Indels 11; Gaps 3;

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QY 3 AAMDVTPSGTSGAGKRFKNNVAVLWMDIVDNCACRHHNDLCTECQANQ 51
DB 2 ATLDSDVTVFPAEGASSSGPSSSTKKPRFEIKKNNVSLWMDIVDNCACRHHNDLCTECQANQ 61

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QY 52 LCIECQANQASATSECTVAMGVGNHAFHFCISRWLKTROVCPDLNREWEFOKYGH 108
DB 62 LCIECQANQASATSECTVAMGVGNHAFHFCISRWLKTROVCPDLNREWEFOKYGH 118

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RESULT 5
US-10-424-599-221431
; Sequence 221431, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 221431
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_41982C.1.pep
US-10-424-599-221431

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Thu Mar 25 10:42:33 2004

us-09-914-324a-1.rapb

Page 3

Query Match 82.2%; Score 506.5; DB 12; Length 152;
Best Local Similarity 80.0%; Pred. No. 2.5e-48;
Matches 92; Conservative 4; Mismatches 10; Indels 9; Gaps 2;
QY 3 AAMVDPT---SGTNSGAG-----KKRFVKKNNAVALMWDIVDNCACRHHIMDL 53
DB 38 ATLSDVPMVPAAGEPSSAGPSSKKPKRFEIKKNNAVALMWDIVDNCACRHHIMDL 97
QY 54 IECQANQASATSECTVAMGVCMNAHFHFCISRWLKTROVCPDLNREMEFOKYGH 108
DB 98 IECQANQASATSECTVAMGVCMNAHFHFCISRWLKTROVCPDLNREMEFOKYGH 152

RESULT 6
US-10-424-599-148915
Sequence 148915, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285864
SEQ ID NO 148915
LENGTH: 106
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(106)
OTHER INFORMATION: unsure at all Xaa locations
OTHER INFORMATION: Clone ID: PAT_MRT3847_105493C.1.pdp
US-10-424-599-148915

Query Match 68.3%; Score 420.5; DB 12; Length 106;
Best Local Similarity 69.2%; Pred. No. 6.1e-39;
Matches 81; Conservative 5; Mismatches 8; Indels 23; Gaps 4;
QY 3 AAMVDPT---PSG-TNSGAG-----KKRFVKKNNAVALMWDIVDNCACRHHIMDL 51
DB 2 ATLSDVPMVPAAGEPSSAGPSSSTKPKRFEIKKNNAVALMWDIVDNCACRHHIMDL 61
QY 52 LCECQANQASATSECTVAMGVCMNAHFHFCISRWLKTROVCPDLNREMEFOKYGH 108
DB 62 LCECQANQASATSECTVAMGVCMNAHFHFCISRWLKTROVCPDLNREMEFOKYGH 106

RESULT 7
US-10-424-599-230014
Sequence 230014, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285864
SEQ ID NO 230014
LENGTH: 75
TYPE: PRT
ORGANISM: Glycine max

FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_49727C.1.pdp
US-10-424-599-230014
Query Match 50.8%; Score 313; DB 12; Length 75;
Best Local Similarity 81.7%; Pred. No. 3.7e-27;
Matches 58; Conservative 0; Mismatches 11; Indels 2; Gaps 2;
QY 40 DN-CAICRHHIMDL-CIECQANQASATSECTVAMGVCMNAHFHFCISRWLKTROVCPDL 97
DB 5 DNICARHSHGFSASECQANQASATSECTVAMGVCMNAHFHFCISRWLKTROVCPDL 64
QY 98 NREMEFOKYGH 108
DB 65 NSEMEFOKYGH 75

RESULT 8
US-09-764-864-826
Sequence 826, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 826
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-864-826

Query Match 47.4%; Score 292; DB 9; Length 118;
Best Local Similarity 50.5%; Pred. No. 1.3e-24;
Matches 49; Conservative 14; Mismatches 30; Indels 4; Gaps 2;
QY 11 SGTNSGAGKKRFVKKNNAVALMWDIVDNCACRHHIMDLCECQANQASATSECTV 70
DB 25 SGSRKSG-GDKVFSIKKNNAVALMWSWDECTCAICRVQVMDACLRQDAEN---KQEDCVV 80
QY 71 AMGVCMNAHFHFCISRWLKTROVCPDLNREMEFOKYGH 107
DB 81 VMGECHSFRNCMSLWVKQNNRCFLCQDPMVQVRIG 117

RESULT 9
US-09-764-864-1285
Sequence 1285, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1285
LENGTH: 131
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (11)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1285
Query Match 47.4%; Score 292; DB 9; Length 131;

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us-09-914-324a-1.rapb

Page 4

Best Local Similarity 50.5%; Pred. No. 1,4e-24;
Matches 49; Conservative 14; Mismatches 30; Indels 4; Gaps 2;

QY 11 SGTNSGAGKRFYKKNNAVALMAMDIYVNDCAICGNHIMDLCEQANQASATSECTV 70
DB 38 SGTSG-GDKMFSLKKNNAVALMAMSWDVCDTCACICRVQVMDACLRQAHEN---KQEDCV 93
QY 71 AMGCNHAFFHCISRMLKTRQVCPDLNREWEFOKYG 107
DB 94 VMGECNHSFHNCCMSLWVKQNNRCPLCQGDWVVOIG 130

RESULT 10

US-10-424-599-238320
; Sequence 238320, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 238320
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_57228C.1.pep
US-10-424-599-238320

Query Match 46.6%; Score 287; DB 12; Length 64;
Best Local Similarity 77.8%; Pred. No. 2,4e-24;
Matches 49; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 45 CRNHIMDLCEQANQASATSECTVAMGCNHAFFHCISRMLKTRQVCPDLNREWEFO 104
DB 1 CRNHIMDLCEQANQASATSECTVAMGCNHAFFHCISRMLKTRQVCPDLNREWEFO 60

QY 105 KYG 107
DB 61 KYG 63

RESULT 11

US-09-826-312-8
; Sequence 8, Application US/09826312
; Patent No. US20020042083A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; TITLE OF INVENTION: UBIQUITIN LIGASE ASSAY
; FILE REFERENCE: A-68613-1/RMS/JUD
; CURRENT APPLICATION NUMBER: US/09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 09/542,497
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-312-8

Query Match 46.6%; Score 287; DB 9; Length 113;
Best Local Similarity 49.5%; Pred. No. 4,3e-24;

Matches 48; Conservative 14; Mismatches 31; Indels 4; Gaps 2;

QY 11 SGTNSGAGKRFYKKNNAVALMAMDIYVNDCAICGNHIMDLCEQANQASATSECTV 70
DB 20 SGTSG-GDKMFSLKKNNAVALMAMSWDVCDTCACICRVQVMDACLRQAHEN---KQEDCV 75
QY 71 AMGCNHAFFHCISRMLKTRQVCPDLNREWEFOKYG 107
DB 76 VMGECNHSFHNCCMSLWVKQNNRCPLCQGDWVVOIG 112

RESULT 12

US-10-108-767-8
; Sequence 8, Application US/10108767
; Publication No. US20030104474A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; TITLE OF INVENTION: ASSAYS FOR IDENTIFYING UBIQUITIN AGENTS AND FOR IDENTIFYING AGENT
; TITLE OF INVENTION: MODIFY THE ACTIVITY OF UBIQUITIN AGENTS
; FILE REFERENCE: A-68613-5/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/108,767
; PRIOR FILING DATE: 2002-09-26
; CURRENT APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 10/091,139
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-767-8

Query Match 46.6%; Score 287; DB 14; Length 113;
Best Local Similarity 49.5%; Pred. No. 4,3e-24;
Matches 48; Conservative 14; Mismatches 31; Indels 4; Gaps 2;

QY 11 SGTNSGAGKRFYKKNNAVALMAMDIYVNDCAICGNHIMDLCEQANQASATSECTV 70
DB 20 SGTSG-GDKMFSLKKNNAVALMAMSWDVCDTCACICRVQVMDACLRQAHEN---KQEDCV 75
QY 71 AMGCNHAFFHCISRMLKTRQVCPDLNREWEFOKYG 107
DB 76 VMGECNHSFHNCCMSLWVKQNNRCPLCQGDWVVOIG 112

RESULT 13

US-10-152-156-8
; Sequence 8, Application US/10152156
; Publication No. US20030108947A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; TITLE OF INVENTION: ASSAYS FOR IDENTIFYING UBIQUITIN AGENTS AND FOR IDENTIFYING AGENT
; TITLE OF INVENTION: MODIFY THE ACTIVITY OF UBIQUITIN AGENTS
; FILE REFERENCE: A-68613-6/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/152,156
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 10/091,174
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 10/091,139

PRIOR FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: US 10/109,460
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 10/108,767
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/291,836
PRIOR FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-10-152-156-8

Query Match 46.6%; Score 287; DB 14; Length 113;
Best Local Similarity 49.5%; Pred. No. 4.3e-24;
Matches 48; Conservative 14; Mismatches 31; Indels 4; Gaps 2;

QY 11 SCNSGAGKRRFVKKNAVALMADIVDNCACIENHMDICIQANQASATSECTV 70
DB 20 SGTSG-GDKFSLKKNPVAWMSWVEDCTCAICVQVMDACLRQAE--KQEDCV 75
QY 71 AMGVCHAFHFCISRWLKTRQVCPDNRNEMEFQKYG 107
DB 76 VMGECHHSFHCMSLWVKNNRCPLQCDMWVYGRIG 112

RESULT 14
US-10-424-599-242288
Sequence 242288, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 242288
LENGTH: 68
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(68)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_60814C.1.pep
US-10-424-599-242288

Query Match 45.8%; Score 282; DB 12; Length 68;
Best Local Similarity 69.1%; Pred. No. 9.1e-24;
Matches 47; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 24 VKKNAVALMADIVDNCACIENHMDICIQANQASATSECTVAMGVCHAFHFC 83
DB 1 IKNCNAGIWMADLVGNCAICRHVWDLVCIDLANQASSTSECTVARGVNHAIHLHC 60
QY 84 ISRWLKTR 91
DB 61 ICRWVXTR 68

RESULT 15
US-10-424-599-264079
Sequence 264079, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 264079
LENGTH: 40
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(40)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_80484C.1.pep
US-10-424-599-264079

Query Match 37.0%; Score 228; DB 12; Length 40;
Best Local Similarity 95.0%; Pred. No. 5.2e-18;
Matches 38; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 69 TVAMGVCHAFHFCISRWLKTRQVCPDNRNEMEFQKYG 108
DB 1 TVAMGVCHAFHFCISRWLKTRQVCPDNRNEMEFQKYG 40

Search completed: March 25, 2004, 09:41:51
Job time : 42 secs